

181547

115

STIC-Biotech/ChemLib

From: Ibrahim, Medina A.  
Sent: Tuesday, March 07, 2006 10:40 AM  
To: STIC-Biotech/ChemLib  
Subject: 10/656,394

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Please do an interference search of the following:

1. DNA encoding SEQ ID NO: 8.
2. SEQ ID NO: 7. Thanks

Medina A. Ibrahim  
Patent Examiner, GAU-1638  
transgenic plants and plant breeding  
Remsen-2B07  
mailbox-2C18  
(571) 272-0797

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 18:59:29 ; Search time 531 Seconds  
(without alignments)  
10374.131 Million cell updates/sec

Title: US-10-656-394A-7  
Perfect score: 3099  
Sequence: 1 atggcgagacgtgtgag.....gcacagctcaagtgctgta 3099

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/6H COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq: \*  
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8: /cgn2\_6/ptodata/1/ina/RE COMB.seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.6	4.0	3925	US-09-330-330-2	Sequence 2, Appli
2	106.6	3.4	10322	US-09-330-330-3	Sequence 3, Appli
3	81.6	2.6	5113	US-09-336-946B-3	Sequence 68, Appl
4	81.6	2.6	5222	US-09-336-946B-68	Sequence 57, Appl
5	81.6	2.6	5222	US-09-993-170-57	Sequence 60, Appl
6	81.6	2.6	5696	US-09-993-170-60	Sequence 1, Appli
7	81.6	2.6	5757	US-09-336-946B-1	Sequence 56, Appl
8	81.6	2.6	5757	US-09-993-170-56	Sequence 4, Appli
9	62.6	2.0	2718	US-09-360-186-4	Sequence 2, Appli
10	62.6	2.0	2718	US-09-864-680A-4	Sequence 2, Appli
11	62.6	2.0	3099	US-09-360-186-2	Sequence 2, Appli
12	62.6	2.0	3099	US-09-864-680A-2	Sequence 1, Appli
13	62.6	2.0	31491	US-09-360-186-1	Sequence 1, Appli
14	62.6	2.0	31491	US-09-864-680A-1	Sequence 2, Appli
15	57.4	1.9	3997	US-08-947-823-2	Sequence 1, Appli
16	57.4	1.9	51952	US-08-947-823-1	Sequence 1, Appli
17	52.8	1.7	5475	US-08-680-327-1	Sequence 3, Appli
18	52.8	1.7	5475	US-09-228-246-3	Sequence 2, Appli
19	52.8	1.7	10968	US-08-680-327-2	Sequence 1, Appli
20	52.8	1.7	10968	US-09-228-246-1	Sequence 1, Appli
21	50.6	1.6	4946	US-08-930-996A-1	Sequence 14, Appl
22	50.4	1.6	7218	US-08-232-463-14	Sequence 70, Appl
23	49.8	1.6	4163	US-09-004-838-70	Sequence 1, Appli
24	49.8	1.6	4208	US-09-004-838-1	Sequence 1, Appli

25	49.4	1.6	3982	3	US-08-947-823-4	Sequence 4, Appli
26	49.4	1.6	9870	3	US-09-245-928A-15	Sequence 15, Appli
27	49	1.6	3741	3	US-09-803-286A-1	Sequence 1, Appli
28	46.6	1.5	1662	3	US-09-004-838-6	Sequence 6, Appli
29	46.2	1.5	2353	3	US-09-004-838-2	Sequence 22, Appli
30	45.4	1.5	1141	3	US-09-806-708B-22	Sequence 15, Appli
31	44.2	1.4	3635	2	US-08-588-983-15	Sequence 15, Appli
32	44.2	1.4	3635	2	US-08-588-976-15	Sequence 22, Appli
33	43.8	1.4	1141	3	US-09-806-708B-22	Sequence 157, App
34	43.6	1.4	5134	3	US-08-310-912A-157	Sequence 157, App
35	43.6	1.4	5134	3	PCT-US95-04589-157	Sequence 3, Appli
36	43.6	1.4	5134	6	US-09-004-838-3	Sequence 128, App
37	40.6	1.3	1036	3	US-09-004-838-128	Sequence 2813, Ap
38	40.2	1.3	1038	3	US-09-621-976-2813	Sequence 109, App
39	39.8	1.3	832	3	US-09-621-976-2813	Sequence 16369, A
40	39	1.3	832	3	US-09-004-838-109	Sequence 7366, Ap
41	38.4	1.2	5829	3	US-09-949-016-16369	Sequence 22648, A
42	38.4	1.2	136917	3	US-09-270-767-7366	Sequence 33950, A
43	38	1.2	478	3	US-09-270-767-22648	
44	38	1.2	478	3	US-09-949-016-33950	
45	38	1.2	601	3		

ALIGNMENTS

RESULT 1  
US-09-330-330-2  
Sequence 2, Application US/09330330  
Patent No. 6274789  
GENERAL INFORMATION:  
APPLICANT: Yano, Masahiro  
APPLICANT: Iwamoto, Masao  
APPLICANT: Katayose, Yuichi  
APPLICANT: Sasaki, Takuji  
APPLICANT: Wang, Zi-Xuan  
APPLICANT: Yamanouchi, Utako  
APPLICANT: Ishimaru, Lisa  
TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,330  
FILING DATE: 11-JUN-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 10-181455  
FILING DATE: 12-JUN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Ph.D., J.D., Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 06501/032001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3925 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:

NAME/KEY: Coding Sequence  
LOCATION: 82...3696  
US-09-330-330-2

Query Match 4.0%; Score 122.6; DB 3; Length 3925;

Best Local Similarity 45.9%; Pred. No. 1.4e-26;

Mismatches 545; Conservative 0; Mismatches 624; Indels 18; Gaps 3;

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QY 800 CTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTTCTTCTTCTAGATCATCTAT 859
DB 1472 CTGGCAGTTGAAAGGCTTTAGAAAAGAAAGTTGCTTGTGTTCTAGATGTTCT 1531
QY 860 GGATTTTACATGATGGAAATGGAATGAAATGCAATTCCTTAAGAACCAATGAAGG 919
DB 1532 CAGATACCTCAGATGGGAGCAGATAAACCAACGTTATTCCTCCCTGTTGGAAGACAA 1591
QY 920 GCATCGAATAGTAATTAACCACTCGGNATGTTGATCTTGGCGAGAAGTGTCCACAGCT 979
DB 1592 GCCGAATATTTGACTACAGAAAGAGATTTTGGCAACATTTGCTCAGGAAATG 1651
QY 980 CACTGGTGTACCACTTTGATTTCTTGCAGATGAACGATGCCATTAACATTTGCTACTGAGA 1039
DB 1652 GAAATGTGCACCACTTTAAAGTTCTTAACATAATGATGTCATTTGTCCTCTTGTAGTGAGA 1711
QY 1040 AAACAAATAAATATCATGAGACATGGAATCAATTAATAAATA-----TGCAAGATGG 1093
DB 1712 AGGATTTTGGAGGGCTACATATTTGGATGATGACAAACATCCAGAGTTGTTAAGAG 1771
QY 1094 TTGAACGAATTTGAATTAATTTGTCGTCTACATTAAGCATGCTTCAATTAACATAGGCTG 1153
DB 1772 CAATAACAACTTAAGAGTGGATGGACTGCTCCCTTGCATATGTTGTCATAGTGGAT 1831
QY 1154 TGCTTGCATTAACAGGTGTC-----AGATGGGAGAAATCTATGAACACCTTCTT 1207
DB 1832 TCTTGGCAACCGCAACACCCAGAGAGAGTGGAGAAATTTGAACGAGATTAATCAATG 1891
QY 1208 CAGAACTAGAAATAAACCCAGCTCGAAGCTTTTGAAGAGATGTTGACCCCTAGTTTACA 1267
DB 1892 CTGAGTTGGAATGATCCAGAGCTTGGATGATAAGAACCGTCTCTGAAAAAGCTATG 1951
QY 1268 ACCACTACCATCCATTTGAAACCACTGCTTTTGTATCTAAGTATCTTCTGAGATT 1327
DB 1952 ATGTTTACCATACATCTCAAGTCATGTTTTTATATCTGTCATTTTCTCCCTGAGACC 2011
QY 1328 TTGAATCAAAAGGAATCGTCTAGTAGTAGATGAGTAGCAGAGGGTTTGTAGACAA 1387
DB 2012 AGATCATTTAGTCGAAGCGTTTGGTGCATGCTTGGCGAGCAGAGGTTACTCAACTGCAG 2071
QY 1388 AGTTGGATGACGACATGAAGATGCGGAGAAATTTCTTTAATGAGCTATCAACGAA 1447
DB 2072 CACATGGGAATCTGCCAATAGTAATAGCTAAGCGCTACTTCAATGAACTCAAGATGAA 2131
QY 1448 GTATGATTTCAACGAT-----CAAGAGTGGCATAGCAGGAAATAAAGACTTTGTCGAA 1501
DB 2132 GCATGATTTTACCATTTCCAGCAATCAGTAGCAGCAGGAAATCAATTTCACTTTGCAAG 2191
QY 1502 TTGATGATATCATCGTGATATCAAGTTTCAATCTCGAGCAGGAAATTTTGTATAT 1561
DB 2192 TCCATGATCTCATGCGTGATCGCCATCTCAAGTCAACGGAGGAAACCTTTGTTT 2251
QY 1562 TACCAATGGAGATGGCTCTGATTTAGTTTCAGGAAACACCTGCCACATAGCATTCATG 1621
DB 2252 GGGTGGAGGAGGCTGCAGCGCTACATACATGTTGTCATCTTCTCTAAGTA 2311
QY 1622 GGATATGCTCTGAAACCTGGATTTGATTTGGAGCAATTTTCGATCATCTATTTTGG 1681
DB 2312 GCAACTGGAAGGAGATAGAGTGAATTCGAGGCGCATAGTGGAATCTGCCGAAATGAT 2371
QY 1682 GTGACAGACCCCAAGCTTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1741
DB 2372 GCTTATCTCTGTTGGGATTTGGAAGCCATTTTTTTTGTATGGAAGATGAGTTTATAC 2431
QY 1742 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCACCGTATTCAT 1801
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DB 2432 GAGTGTGCTTGAAGGAGCTAGAGGCTTAGAATATCATCACCTTGTGATCAGATTTGGA 2491
QY 1802 TGTGTGCGCACTTGAATATCTTGAATATTTGATATTTCTCATCATATATTTCACTTCCA 1861
DB 2492 AGCTTAATCACTTAAATTTCTTTCTTCTACGAGGATGCTATGCTATTTGATCTACTGCCAG 2551
QY 1862 GATCCATTTGTTAACTTACAGGGCCTTACAACTTTTGAACATGCCGAGCACAATATTCGAG 1921
DB 2552 ATTACTGGGCACTTACGAGCACTTCCAGATGCTAGACATCAGAGGTACATATGTAAGG 2611
QY 1922 CACTACCACTGAGATCAGTAACTTCAATGCTCTGCTACTTCTTCTTCTTCTTCTTCTTCT 1968
DB 2612 CTTTGCCAAAAACCATCATCAAGCTTCAAGAGCTACAGTACATTCAT 2658
```

## RESULT 2

US-09-330-330-3

; Sequence 3, Application US/09330330

; Patent No. 6274789

; GENERAL INFORMATION:

; APPLICANT: Yano, Masahiro

; APPLICANT: Iwamoto, Masao

; APPLICANT: Katayose, Yuichi

; APPLICANT: Sasaki, Takuji

; APPLICANT: Wang, Zi-Xuan

; APPLICANT: Yamanouchi, Utako

; APPLICANT: Ishimaru, Lisa

; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/330,330

; FILING DATE: 11-JUN-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 10-181455

; FILING DATE: 12-JUN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Ph.D., J.D., Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 06501/032001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1032 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

; US-09-330-330-3

Query Match 3.4%; Score 106.6; DB 3; Length 10322;

Best Local Similarity 46.5%; Pred. No. 2.9e-21;

Mismatches 423; Conservative 0; Mismatches 474; Indels 12; Gaps 2;

QY 1072 AATAAAATATGCAAAAGATGTTGAAAGATTTGAAATTAATATGTTGCTTACCATTA 1131

DB 7027 AATCCAGAGTTGGTTAAAGAGCAAAACAAATCTTAAAGAGATGCGATGCGCTT 7086

QY 1132 GCAATCTTACATAGGAGCTGTGTTGCAACTAAACAGGTGTC-----AGAAATGGAG 1185

Db 7087 GCAATAGTGTCTAGTGGTATCTTTGGCAACACCGACCAAGACCCAGAGAGTGGAGA 7146  
Qy 1186 AAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAACCACCAAGCTTGGAGCTTTCAGG 1245  
Db 7147 AAATTTGAACGAGATATCAATGCTGAGTTGGAAATGAATCCAGAGCTTGGATGATAGA 7206  
Qy 1246 AGAATGGTGACCTTAGGTATCAACACCTACATCCATCCATTTGAAACCAAGCTTTTGTAT 1305  
Db 7207 ACCGTCCTTGAAGAAAGCTATGATGCTTTTACCATCCTTCAAGTCAATGTTTTTATAT 7266  
Qy 1306 CTAAGTATCTTCTGAGGATTTTGAATCAAAAGAAATCGTCTAGTAGGTAGATGATA 1365  
Db 7267 CTGTCCATTTTCCCTGAGACCAAGATCATTTAGTCGAGGCGTTTGGTGCATCTGTTGGCA 7326  
Qy 1366 GCAGAGGGTTTGTAGACCAAGGTGGGATGACGACTTAAGGATGTCCGGAAGAAAGTTAC 1425  
Db 7327 GCAGAGGTTTACTCACTGACGACATCGGAAATCTGCCATTTGAAATAGCTAACGGCTAC 7386  
Qy 1426 TTTAATGAGCTATCAACCAAGTATGATTTCAAGCAT-----CAAGAGTGGCATGCA 1479  
Db 7387 TTTAATGAGCTATCAACCAAGTATGATTTCAAGCATTTTACCATTTCCAGCAATCAGGTAGCGAGG 7446  
Qy 1480 GGAATAATTAAGACTTGTGCAATTCATGATATCATCCGATATATCAGATTTTCAATCTCG 1539  
Db 7447 AAATCAATGACTCTTGCAAGTCCATGATCTCATGCGGTGACATCGCCATCTCAAGTCA 7506  
Qy 1540 AGACAGGAAATTTGTATTTATTTACCAATGGGAGATGCTGATTTAGTTTACAGGAAAC 1599  
Db 7507 ACGGAGAAACCTTTGTTTGGGTGGAGGAGGCTGCGCGGTACATACATGATGTCGA 7566  
Qy 1600 ACTGCCACATAGCATTTCCATGGGAGTATGCTCGCAAACTGGGATTTGGAGCATTT 1659  
Db 7567 ATTGCTCATCTGTCTATAGTCAACTGGAAGGAGATAGAGTGAATTCGAGGCGATA 7626  
Qy 1660 ATTGCATATAGCTATTTTGTGACAGACCAAGAGCTTAGCAGATGAGTTTGTCCA 1719  
Db 7627 GTGACCTGTCCCGAATACGATCGTTTATCTCTGTTTGGGGATTTGGAAGCCATTTTGT 7686  
Qy 1720 GATCAATTTGAGGATTTTACGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAA 1779  
Db 7687 TATGCAAGATGAGTTTATACAGTGTCTGACTTTGAAGGAGCTAGAGGCTAGATAT 7746  
Qy 1780 AAGATTTGACCGTATGATGTTTGTGCGACTTGAATATCTTGAATGATGATTTTCG 1839  
Db 7747 CATCACTTGTATGAGTTTGAAGCTTAAATCACTTAAATTTCTTCTACGAGGATGC 7806  
Qy 1840 TCATCCATATATTCATCTCCAGATCCATTTGGTAAACTACAGGCGCTACAACTTTGAAC 1899  
Db 7807 TATCGTATGATCTGACAGATTTTACTGGGCACTTGGGCACTTCCAGATGCTAGAC 7866  
Qy 1900 ATGCCGAGCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1959  
Db 7867 ATCAGAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7926  
Qy 1960 ACTCTCTGT 1968  
Db 7927 TACATCAT 7935

RESULT 3  
US-09-336-946B-3  
; Sequence 3, Application US/09336946B  
; Patent No. 6479731  
; GENERAL INFORMATION:  
; APPLICANT: Valent, Barbara S.  
; APPLICANT: Bryan, Gregory  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: A PI-TA GENE CONFERRING DISEASE RESISTANCE TO PLANTS  
; FILE REFERENCE: BB-1136  
; CURRENT APPLICATION NUMBER: US/09/336, 946B  
; PRIORITY FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 60/095229

; PRIOR FILING DATE: 1998-08-04  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 5113  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-336-946B-3  
  
Query Match 2.6%; Score 81.6; DB 3; Length 5113;  
Best Local Similarity 46.7%; Pred. No. 1.1e-13;  
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;  
  
Qy 908 ACATAGAGGCGAGTCCGAATAGTAATAACCACTCGGAATGTTGATCTTGGCGAGAAGT 967  
Db 3124 ATAATAATAGTTGAGTAGAATACTAATAACACAGAAATTTGAACCTTGTAGCTTTGGCAT 3183  
Qy 968 GTGCCACAGCCTCACTGTGTGTACCACTTGTATTTCTTCAGATGAACGATGCCAATAACAT 1027  
Db 3184 GCTGTGATATAACTCAGAGCACATTTATAGATTGATCCACTGGGTGATGATGCTCAA 3243  
Qy 1028 TGCTACTGAGAAACAAATAAATAATCATGAGACATGATCAATCAATAAATAAATAATGCAA 1087  
Db 3244 GTCAATTTGTTTTCAGTGGAGTTGTTGGCAAGGAAATGAAATTTCTCGGACATTTACTG 3303  
Qy 1088 AGATGGTTGAACGAATTTGTAATAAATGTTGTCGTCTACCACTTAGCAATATCTTACAATAG 1147  
Db 3304 AAGTTTCTCATGACATGATAAATAATGTTGGCTTGGCTTGGCACTAGCAATACTATAACAG 3363  
Qy 1148 GAGCTGTGTTGCACTAAACAGGTGTCAGATGGGAGAAATTTCTATGAACACTT----- 1202  
Db 3364 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAATGGAATCAATACATAAATAAT 3423  
Qy 1203 -----TCCTTCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGATGTTGA 1255  
Db 3424 CATGACTACTTCCATTTGAAGAAATAATCTTCTTTCAGGGGATGAGCAAGTACTCA 3483  
Qy 1256 CCTAGGTATCAACACCTTACCATCCCATTTGAAACCAATGCTTTTGTATTAAGTATCT 1315  
Db 3484 ACCTTATTTACATATATCTTCTCTCAATGTTTGAAGCATGCTGTATATACCTTAGCATCT 3543  
Qy 1316 TTCTGAGGATTTTGAATAAATAAAGCAATCGTCTAGTAGGTAGATGATGATGATGATGATGAT 1375  
Db 3544 ACAAGAGGCTACATATTTAGAGGCGCACTTGGTGGCAATGGATGGCTGAGGTT 3603  
Qy 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAGAAAGTTTACTTTAATGAGC 1435  
Db 3604 TCATCAATTCATAGAAAAATAAAGTCATGGAAGGTTGCAAGGAACTATTTTGTATGAAC 3663  
Qy 1436 TAATCAACCGAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTT 1495  
Db 3664 TTGTTGGTAGGGGCTGCTCCAAACGATGATGTTAACTGCAAAATGAGGATTTGTGAT 3723  
Qy 1496 GTCGAATTCATGATATCATCCGTGATATCAGATTTCAATCTCAGAGAGGAAAAATTT 1553  
Db 3724 GTGTAGTGCACCATGTTTAAATTTTATCACTGAGTGAAGTCAATAGAGGAGAAATTT 3781

RESULT 4  
US-09-336-946B-68  
; Sequence 68, Application US/09336946B  
; Patent No. 6479731  
; GENERAL INFORMATION:  
; APPLICANT: Valent, Barbara S.  
; APPLICANT: Bryan, Gregory  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: A PI-TA GENE CONFERRING DISEASE RESISTANCE TO PLANTS  
; FILE REFERENCE: BB-1136  
; CURRENT APPLICATION NUMBER: US/09/336, 946B  
; PRIORITY FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 60/095229  
; NUMBER OF SEQ ID NOS: 74





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; LENGTH: 5757
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric Gene
US-09-993-170-60

Query Match      2.6%; Score 81.6; DB 3; Length 5757;
Best Local Similarity 46.7%; Pred. No. 1.2e-13;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

QY 908 ACAATAAGAGGGCAGTCGAATAGTAATAACACCTCGGAATGTTGATCTTCGCGAGAAGT 967
DB 3438 ATAATAATAGTTGCGAGTAGATTAATAACACAGAAATGAACCTGTAGCTTTGGCAT 3497
QY 968 GTGCCACAGCCTCAGTGGTGTACCACTTGAATTCCTTCAGATGAAGATGCCATAACAT 1027
DB 3498 GCTGTGGATATACTCAGAGCACATTAATTAAGATTGATCCACTGGGTGATGATGCTCAA 3557
QY 1028 TGCTACTGAGAAACAAATATAAATCATGAAGACATGGAATCAAAATAAAATATGCAA 1087
DB 3558 GTCAATTTGTTTTCAGTGGAGTTGTTGGCCAAAGGAATGAATTTCTTGGACATCTTACTG 3617
QY 1088 AGATGGTTGAACGAATGTAATAAATAATGTTGGTCTACCAATAGCAATATCTTCAATAG 1147
DB 3618 AAGTTTCTCATGATGATATAAATAATGTTGGTCTTGCCTACTAGCAATATCTATAACAG 3677
QY 1148 GAGCTGTGCTTGCACACTTAACAGGTTGTCAGATGGGAGAAATTTCTATGAACACCT----- 1202
DB 3678 CCAGACATNTTAAAGCCAGCTGTTAGATGGATGCGAATGGATCATACATACAAAAT 3737
QY 1203 -----TCCTTCAGAACTAGAAATAAACCCAGCTCGGAAGCTTTGAGGAGAAATGTGA 1255
DB 3738 CATGACTACTTCCAAATTTGAAGAAATCTTACTTTGCGGGGATGAGGCAAGTACTCA 3797
QY 1256 CCCTAGGTACACCACTACCATCCATTTGAAACCATGCTTTTGTATCTTAAGTATCT 1315
DB 3798 ACCTATTATCAATAATCTTCTCTCTGTTTGAAGAGCATGCTGTATATACCTTAGCATCT 3857
QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1375
DB 3858 ACAAGAGGACTACATAATTTAGGAGGCCAACTTGTGAGGCAATGGATGCTGAAGGTT 3917
QY 1376 TTGTTAGACCAAGTATGATTCAACGATCAAGATGGGATGAGTAACTGCAAAATAGGATTT 1435
DB 3918 TCATCAATCCATAGAAATAAAGTCAATGGAAGAGTTGCGAGGAACTATTTTGTATGAC 3977
QY 1436 TAATCAACCGAAGTATGATTCAACGATCAAGATGGGATGAGGCAATTAAGACTT 1495
DB 3978 TTGTTGTTAGGGGCTGCTCCACAGTAGATGTTAACTGCAAAATAGGATTTGTGAT 4037
QY 1496 GTCGAATTCATGATATATCATCCGATATACAGTTTCAATCTCGAGACAGGAAATTT 1553
DB 4038 GTGTAGTGCACCATGTTATTAATTTTCAATCAGGTGAAGTCAATAGAGGAGAAATTT 4095

RESULT 7
US-09-336-946B-1
; Sequence 1, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: A P-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336, 946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1

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; LENGTH: 5757
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric Gene
US-09-993-170-60

Query Match      2.6%; Score 81.6; DB 3; Length 5696;
Best Local Similarity 46.7%; Pred. No. 1.2e-13;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

QY 908 ACAATAAGAGGGCAGTCGAATAGTAATAACACCTCGGAATGTTGATCTTCGCGAGAAGT 967
DB 3438 ATAATAATAGTTGCGAGTAGATTAATAACACAGAAATGAACCTGTAGCTTTGGCAT 3497
QY 968 GTGCCACAGCCTCAGTGGTGTACCACTTGAATTCCTTCAGATGAAGATGCCATAACAT 1027
DB 3498 GCTGTGGATATACTCAGAGCACATTAATTAAGATTGATCCACTGGGTGATGATGCTCAA 3557
QY 1028 TGCTACTGAGAAACAAATATAAATCATGAAGACATGGAATCAAAATAAAATATGCAA 1087
DB 3558 GTCAATTTGTTTTCAGTGGAGTTGTTGGCCAAAGGAATGAATTTCTTGGACATCTTACTG 3617
QY 1088 AGATGGTTGAACGAATGTAATAAATAATGTTGGTCTACCAATAGCAATATCTTCAATAG 1147
DB 3618 AAGTTTCTCATGATGATATAAATAATGTTGGTCTTGCCTACTAGCAATATCTATAACAG 3677
QY 1148 GAGCTGTGCTTGCACACTTAACAGGTTGTCAGATGGGAGAAATTTCTATGAACACCT----- 1202
DB 3678 CCAGACATNTTAAAGCCAGCTGTTAGATGGATGCGAATGGATCATACATACAAAAT 3737
QY 1203 -----TCCTTCAGAACTAGAAATAAACCCAGCTCGGAAGCTTTGAGGAGAAATGTGA 1255
DB 3738 CATGACTACTTCCAAATTTGAAGAAATCTTACTTTGCGGGGATGAGGCAAGTACTCA 3797
QY 1256 CCCTAGGTACACCACTACCATCCATTTGAAACCATGCTTTTGTATCTTAAGTATCT 1315
DB 3798 ACCTATTATCAATAATCTTCTCTCTGTTTGAAGAGCATGCTGTATATACCTTAGCATCT 3857
QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1375
DB 3858 ACAAGAGGACTACATAATTTAGGAGGCCAACTTGTGAGGCAATGGATGCTGAAGGTT 3917
QY 1376 TTGTTAGACCAAGTATGAGTACGATCAAGATGGGATGAGTAACTGCAAAATAGGATTT 1435
DB 3918 TCATCAATCCATAGAAATAAAGTCAATGGAAGAGTTGCGAGGAACTATTTTGTATGAC 3977
QY 1436 TAATCAACCGAAGTATGATTCAACGATCAAGATGGGATGAGTAACTGCAAAATAGGATTT 1495
DB 3978 TTGTTGTTAGGGGCTGCTCCACAGTAGATGTTAACTGCAAAATAGGATTTGTGAT 4037
QY 1496 GTCGAATTCATGATATATCATCCGATATACAGTTTCAATCTCGAGACAGGAAATTT 1553
DB 4038 GTGTAGTGCACCATGTTATTAATTTTCAATCAGGTGAAGTCAATAGAGGAGAAATTT 4095

RESULT 8
US-09-993-170-56
; Sequence 56, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 56
; LENGTH: 5757

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[illegible]



Db 847 TAAAGAGAAAGAGTACTTAATTTCTTGGATGATATCTGGATTGTGAAGTGGGATG 906  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTCGAATAGTAATACCA 940  
Db 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGAGGAGTCGAATAGTGTGACTA 963  
QY 941 CTCGGAATGTTGATCTTGGCGGAGAGTGTGCACAGCCTCACTGGTGTACCACTTGAT 1000  
Db 964 CCGTATGATGAAGTAGCTTGTATGCTGTGTAGAGAAATTTCTTTCGGATGAGCT 1023  
QY 1001 TCTTGCAGATGAAGATGCGAATAAATTTGCTACTAGAGAAACAATAAATATCATGAAG 1060  
Db 1024 TCATGGATCAAGATGAGAGTGTGAGTCTTTTCAAAGTGCAGCAATTTTCAAGTGA----- 1078  
QY 1061 ACATGGAATCAATATAAATAATGCAAAAGATGTTGAAGCAATTTGTAATAAATGTGGTC 1120  
Db 1079 ----AGATTACCATATGAGTTCGAGACTGTTGGAAAGCAATCGCAGATGATGTCAAG 1134  
QY 1121 GTCTACATATGACAACTACTTACAAATAGGAGTGTGCTTGGCACTAAACAGGTGCAAGAT 1180  
Db 1135 GGTACCACCTAACTATTTGCTGTGTGAGGCTTCTCAAATCTAAAGAGCAATAGAG 1194  
QY 1181 GGGAGAAATCTATGAACACTTCTTTCAGAACTAGAAATAAACCAGCCTGGAAGCT 1240  
Db 1195 ATTGGAATCTGTTGCTAAAGATGTCAGTCAATGTCACAAATGATCCTGATGAGAT 1254  
QY 1241 TGAGGAGATGTTGACCTAGTGTACAACTACCACTACCACTTCCATTTGAAACCATGCTTTT 1300  
Db 1255 GTTCAGTGTGCTTGGGTTGAGTTAGCATCACTTGCACAGGAGTCTAAACCATGCTTTC 1314  
QY 1301 TGTATCTAATGATCTTCTGAGGATTTTGAATCAAAAGCAATCGTCTAGTAGGTAGAT 1360  
Db 1315 TGCATTCGGAATTTTCCAGAGACAGTGAATTTCCAGTGAAGATTTGATGATCAT 1374  
QY 1361 GGATGAGAGAGGTTTGTGTA 1381  
Db 1375 GGATGGCTGAGGGGTTCTCTGA 1395

RESULT 13  
US-09-360-186-1  
; Sequence 1, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; EARLIER FILING DATE: 1999-07-23  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 31491  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
US-09-360-186-1

Query Match 2.0%; Score 62.6; DB 3; Length 31491;  
Best Local Similarity 47.2%; Pred. No. 3.7e-07;  
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;  
QY 821 TCAAGGAGAGAGGAGTACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAAT 880  
Db 2234 TAAAGAGAAAGAGGAGTACTTAATTTGTTCTGGATGATATCTGGAGTTGTGAAGTGTGGGATG 2293  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTCGAATAGTAATACCA 940  
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGAGGAGTCGAATAGTGTGACTA 2350  
QY 941 CTCGGAATGTTGATCTTGGCGGAGAGTGTGCACAGCCTCACTGGTGTACCACTTGAT 1000

Db 2351 CCGTAAATGATGAAGTAGCTTGTATGCTGCTGTAGAGAAATTTTCTTTCGGATGAGCT 2410  
QY 1001 TCTTGCAGATGAACGATGCCATAACAATTTGCTACTAGAGAAACAATAAATCATGAAG 1060  
Db 2411 TCATGATCAAGATGAGAGTGTGGAGTCTTTTCAAAGTGCAGCAATTTTCAAGTGA----- 2465  
QY 1061 ACATGGAATCAATATAAATAATGCAAAAGATGTTGAAGCAATTTGTAATAAATGTGGTC 1120  
Db 2466 ----AGCATTTACCATATGAGTTCGAGACTGTTGGAAAGCAATCGCAGATGATGTCAAG 2521  
QY 1121 GTCTACATATGCAATACTTACAAATAGGAGTGTGCTTGGCACTAAACAGGTGCAAGAT 1180  
Db 2522 GGTACCACCTAACTATTTGCTGTGTGAGGCTTCTCAAATCTAAAGAGCAATAGAG 2581  
QY 1181 GCGAGAAATCTATGAACACTTCTTTCAGAACTAGAAATAAACCAGCCTGGAAGCT 1240  
Db 2582 ATTGGAAACTGTTGCTAAAGATGTCAGTCAATTCGTCACAAATGATCCTGATGAAGAT 2641  
QY 1241 TGAGGAGATGTTGACCTAGTGTACAACTACCACTACCACTTCCATTTGAAACCATGCTTTT 1300  
Db 2642 GTTCAGTGTGCTTGGGTTGAGTTAGCATCACTTGCACAGGAGTCTAAACCATGCTTTC 2701  
QY 1301 TGTATCTAATGATCTTCTGAGGATTTTGAATCAAAAGCAATCGTCTAGTAGGTAGAT 1360  
Db 2702 TGCATTCGGAATTTTCCAGAGACAGTGAATTTCCAGTGAAGATTTGATGATCAT 2761  
QY 1361 GGATGAGAGAGGTTTGTGTA 1381  
Db 2762 GGATGGCTGAGGGGTTCTCTGA 2782

RESULT 14  
US-09-864-680A-1  
; Sequence 1, Application US/09864680A  
; Patent No. 6762285  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, Brian J  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Tai, Thomas H  
; TITLE OF INVENTION: B2 RESISTANCE GENE  
; FILE REFERENCE: 42250/234021 (5830-4A)  
; CURRENT APPLICATION NUMBER: US/09/864,680A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR FILING DATE: 1999-07-23  
; PRIOR FILING DATE: 1999-07-23  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 31491  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
US-09-864-680A-1

Query Match 2.0%; Score 62.6; DB 3; Length 31491;  
Best Local Similarity 47.2%; Pred. No. 3.7e-07;  
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;  
QY 821 TCAAGGAGAGAGGAGTACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAAT 880  
Db 2234 TAAAGAGAAAGAGGAGTACTTAATTTGTTCTGGATGATATCTGGAGTTGTGAAGTGTGGGATG 2293  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTCGAATAGTAATACCA 940  
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGAGGAGTCGAATAGTGTGACTA 2350  
QY 941 CTCGGAATGTTGATCTTGGCGGAGAGTGTGCACAGCCTCACTGGTGTACCACTTGAT 1000  
Db 2351 CCGTAAATGATGAAGTAGCTTGTATGCTGTGTAGAGAAATTTTCTTTCGGATGAGCT 2410  
QY 1001 TCTTGCAGATGAACGATGCCATAACATTTGCTACTAGAGAAACAATAAATCATGAAG 1060

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Db 2411 TCATGGATCAAGATGAGAGTGTGGAGTCTTTTCAAAAGTCAGCATTTTCAAGTGA----- 2465
Qy 1061 ACATGGAAATCAAAATATATGCAAAAGATGGTTGACGAAATGTAATAAATGTTGTC 1120
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Qy 1121 GTCTACCATTTAGCAATACCTTACAAATAGGAGCTGTGCTTGGCACTTAAACAGGTGTCAAGAT 1180
Db 2522 GGTATACCACTAATATGTCGTGGTTGTCAGGGCTTCTCAATCTTAAAGGACCAATAGAAG 2581
Qy 1181 GGGAGAAATCTATGAACACCTTCTCTCAGAACTAGAAATAAACCCAAAGCTTGAAGCTT 1240
Db 2582 ATTGGAATACTGTGCTTAAAGATGTCAGTCTTCTGTCACAAATGATCTCGATGAACGAT 2641
Qy 1241 TGAGGAGAAATGGTGACCTTAGGTATCAACACCTACCATCCATTTGAAACCAATGCTTTT 1300
Db 2642 GTTCAGCTGTGCTTGGTTGAGTTAGTACGATCACTTGACAAGCGATCTTAAACCAATGCTTTC 2701
Qy 1301 TGTATCTAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360
Db 2702 TGCATTTGGAATTTTTCAGAAAGACAGTGATATTCAGTGAAGAAATTCATGAGATCAT 2761
Qy 1361 GGATAGCAGAAAGGTTTGTGA 1381
Db 2762 GGATGGCTGAGGGTTCCTGA 2782

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RESULT 15

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US-08-947-823-2
; Sequence 2, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kaloshian, Iegouhi
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Pest Resistance in Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3997 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..3852
; OTHER INFORMATION: /note= "Copy 1 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
; US-08-947-823-2

Query Match 1.9%; Score 57.4; DB 3; Length 3997;
Best Local Similarity 51.4%; Pred. No. 3.2e-06;
Matches 161; Conservative 0; Mismatches 146; Indels 6; Gaps 1;

Qy 1241 TGAGGAGAAATGGTGACCTTAGGTATCAACACCTACCATCCCATTTGAAACCAATGCTTTT 1300
Db 2342 TGATGAAAGTTATAGAATTAAGTTATGACCAATTTTACCACATCACCTCAAGCCCATGCTTC 2401
Qy 1301 TGTATCTAAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360
Db 2402 TGTATTTTCAAGTTTTCGAGAGGACACTTCAATTGACAACTATGAGTTGAATGTTATT 2461
Qy 1361 GGATAGCAGAAAGGTTTGTGTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAA 1420
Db 2462 TCGGTGCTGAAGGATTTGTGGGAAAGACGAGATGAACAGTATGGAAGAAAGTGTGGAAGA 2521
Qy 1421 GTTACTTTAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAG 1480
Db 2522 TTTATATGATGATTTAATTTTACAGTAGCTTGGTAATTTGTTTCAATGAG-----ATAG 2575
Qy 1481 GAAAAATTAAAGACTTTGTCGAAATTCATGATATCATCCGTGATATACAGTTTCAATCTCGA 1540
Db 2576 GTTATGCACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTGATAAAGCAA 2635
Qy 1541 GACAGGAAAAATTT 1553
Db 2636 GAAAGGAAAAATTT 2648

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Search completed: March 10, 2006, 00:23:52  
Job time : 535 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 21:27:02 ; Search time 2376 Seconds  
(without alignments)  
10785.691 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3099	100.0	3099	8	US-10-656-394A-7
2	2951.6	95.2	99090	8	US-10-656-394A-13
3	2916.2	94.1	3096	6	US-10-352-179-88
4	2910.2	93.9	3099	8	US-10-656-394A-3
5	2910.2	93.9	3674	8	US-10-656-394A-16
6	2850.2	92.0	3276	6	US-10-352-179-92
7	2820.4	91.0	76272	6	US-10-352-179-83
8	2865.2	82.8	4596	7	US-10-437-963-37316
9	2393.6	77.2	2597	8	US-10-656-394A-11
10	1882	60.7	2982	7	US-10-437-963-2483
11	1621	52.3	2422	8	US-10-656-394A-15
12	1574.2	50.8	3220	6	US-10-352-179-90
13	1562.2	50.4	2940	6	US-10-352-179-84
14	1557	50.2	2925	7	US-10-437-963-41016
15	1553.4	50.1	2982	8	US-10-656-394A-1
16	1170.6	37.8	3024	7	US-10-437-963-7778
17	1143.2	36.9	3492	7	US-10-437-963-49433
18	1133.8	36.6	2982	6	US-10-352-179-86
19	1040.4	33.6	4147	8	US-10-656-394A-5
20	1036.8	33.5	2711	7	US-10-437-963-38603
21	918.8	29.6	2265	6	US-10-352-179-96
22	838.2	27.0	2351	6	US-10-352-179-97
23	546.2	17.6	1355	6	US-10-352-179-94

24	521.8	16.8	2439	7	US-10-437-963-74853	Sequence 74853, A
25	440.8	14.2	2781	7	US-10-437-963-69440	Sequence 69440, A
26	413	13.3	1214	8	US-10-656-394A-14	Sequence 14, Appl
27	381.8	12.3	1389	8	US-10-656-394A-9	Sequence 9, Appl
28	213.4	6.9	569	7	US-10-767-701-21019	Sequence 21019, A
29	198	6.4	4026	7	US-10-437-963-32604	Sequence 32604, A
30	186.6	6.0	2931	7	US-10-437-963-70256	Sequence 70256, A
31	184	5.9	2862	3	US-09-354-453-35	Sequence 35, Appl
32	184	5.9	2862	5	US-10-267-718-35	Sequence 55316, A
33	178.6	5.8	4542	7	US-10-437-963-55316	Sequence 34, Appl
34	176.8	5.7	2954	3	US-09-354-453-34	Sequence 34, Appl
35	176.8	5.7	2954	5	US-10-267-718-34	Sequence 34, Appl
36	176.8	5.7	6760	3	US-09-354-453-33	Sequence 33, Appl
37	176.8	5.7	6760	5	US-10-267-718-33	Sequence 33, Appl
38	172.6	5.6	2373	7	US-10-437-963-48577	Sequence 48577, A
39	172.6	5.6	3012	7	US-10-437-963-78921	Sequence 78921, A
40	171	5.5	2883	7	US-10-437-963-75977	Sequence 75977, A
41	165.8	5.4	3165	7	US-10-425-114-31426	Sequence 31426, A
42	165.8	5.4	3430	8	US-10-425-115-34053	Sequence 34053, A
43	165.6	5.3	2022	7	US-10-437-963-16135	Sequence 16135, A
44	165	5.3	2886	7	US-10-437-963-51200	Sequence 51200, A
45	162	5.2	2981	7	US-10-437-963-98981	Sequence 98981, A

## ALIGNMENTS

RESULT 1  
US-10-656-394A-7  
; Sequence 7, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE REFERENCE: broad-spectrum resistance gene P12  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3099)  
US-10-656-394A-7

Query Match	100.0%	Score 3099;	DB 8;	Length 3099;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3099;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	GCCTCGCTGCTGCCGACGACGACGCTCTCTCTGGCGCTCGAGAAAGACATCTGGTAT	120	
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Qy	121	ATCAAAGATGAGCTAAAAACGATCAAGCAAGCATTCCTTAGAGCTGCTGAACCTATATGAAAAG	180	
Db	121	ATCAAAGATGAGCTAAAAACGATCAAGCAAGCATTCCTTAGAGCTGCTGAACCTATATGAAAAG	180	
Qy	181	AAAGATGAGCTATTAAGGTTTGGCGAGCAATAGCTGACCTGTCATATGACATTGAA	240	
Db	181	AAAGATGAGCTATTAAGGTTTGGCGAGCAATAGCTGACCTGTCATATGACATTGAA	240	
Qy	241	GATTCCTTGTATGAATTTAAGGTCCATATTAAGAAACCAACCTATTTCGTAGTTGGTG	300	
Db	241	GATTCCTTGTATGAATTTAAGGTCCATATTAAGAAACCAACCTATTTCGTAGTTGGTG	300	

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DB 301 AACTCAGAGAACCGCCACCGAATTCGTATCCGTATCCACACCTTAAATCAAGAGTTGAA 360  
QY 361 GAAGTAGTAGCAGAGAACACAGCTACAGTTTGTAGTCAAGCCTATTTCTCTGGCAGAG 420  
DB 361 GAAGTAGTAGCAGAGAACACAGCTACAGTTTGTAGTCAAGCCTATTTCTCTGGCAGAG 420  
QY 421 ATTGACATGATTCCTATCCAGAACATTCGTATCAGTCAGCTCCCAATGCGATGAG 480  
DB 421 ATTGACATGATTCCTATCCAGAACATTCGTATCAGTCAGCTCCCAATGCGATGAG 480  
QY 481 GCTGAGCTGTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
DB 481 GCTGAGCTGTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
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DB 541 GCTAATGATGCTCCGCGCAAGGTAATCTGTGTTGGATGGGTGTTAGCAAGACA 600  
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 2821 GGGCTTGGTCACTCGAGGAGAGAGTGAACGCAACCCAAATCGCCCGTGTGCTTAATG 2880  
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 3061 AATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTGA 3099

RESULT 2

US-10-656-394A-13  
 ; Sequence 13, Application US/10656394A  
 ; Publication No. US20040210957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang et al.  
 ; TITLE OF INVENTION: Cloning and Characterization of the  
 ; TITLE OF INVENTION: Broad-spectrum resistance gene P12  
 ; FILE REFERENCE: 035718/252062  
 ; CURRENT APPLICATION NUMBER: US/10/656,394A  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 99090  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 23215  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-656-394A-13

Query Match 95.2%; Score 2951.6; DB 8; Length 99090;  
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 Matches 2954; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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## RESULT 3

US-10-352-179-88

Sequence 88, Application US/10352179

Publication No. US2004006788A1

GENERAL INFORMATION:

APPLICANT: Wang, Guo-liang

APPLICANT: Liu, Guifu

TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl

FILE REFERENCE: 22727/04108

CURRENT APPLICATION NUMBER: US/10/352,179

CURRENT FILING DATE: 2003-01-27

PRIOR APPLICATION NUMBER: 60/352,106

PRIOR FILING DATE: 2002-01-25

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn version 3.1

SEQ ID NO 88

LENGTH: 3096

TYPE: DNA

ORGANISM: Oryza minuta

FEATURE:

NAME/KEY: CDS



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 Db 2761 GGTATCAATTCACCTTCCAAAGCTCAGGAGATTTCCAAATTTAGATACGGAAGTAAAGTGGCT 2820  
 Qy 2821 GGGTTGGTTCAGCTGAGGAGGAGTGAACGACACCAATTCGCGCGCTGCTGCTTAATG 2880  
 Db 2821 AGGCTTGGTTCAGCTGAGGAGGAGTGAACACACCAATTCGCGCGCTGCTGCTTAATG 2880  
 Qy 2881 TACAGTACCGGAAGTATCAGCACTGGGGCTGAAGCGGAGGATCTTCTATAGAAGTG 2940  
 Db 2881 GACAGTACCGGAAGGATCAGCACTGGGGCTGAAGCGGAGGATCTTCTATAGAAGTG 2940  
 Qy 2941 CAAACAGCAGATCTGTCTCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGCAAG 3000  
 Db 2941 CAAACAGCAGATCTGTCTCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGCAAG 3000  
 Qy 3001 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTGCAGGATGATCAGTGTGACGAGC 3060  
 Db 3001 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTGCAGGATGATCAGTGTGACGAGC 3060  
 Qy 3061 AATGATAGCGAAG 3073  
 Db 3061 AATGATAGCGAAG 3073  
 Qy 3073 AATGATAGCGAAG 3073  
 Db 3073 AATGATAGCGAAG 3073

; Sequence 3, Application US/10656394A  
 ; Publication No. US20040210957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: wang et al.  
 ; TITLE OF INVENTION: Cloning and Characterization of the  
 ; FILE REFERENCE: 035718/252062  
 ; CURRENT APPLICATION NUMBER: US/10/656,394A  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 3099  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(3099)  
 ; US-10-656-394A-3

Query Match 93.9%; Score 2910.2; DB 8; Length 3099;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGACGCTGCTGAGCATGCGAGGTGCTGCTGGGCGAGCGCATCAGCAAGGCC 60  
 Db 1 ATGGCGGAGACGCTGCTGAGCATGCGAGGTGCTGCTGGGCGAGCGCATCAGCAAGGCC 60  
 Qy 61 GCCTCCGCTGTCGCGAGCAGACGACGCTCTCTGCTGGGCGTTCGAGAAAGACATCTGGTAT 120  
 Db 61 GCCTCCGCTGTCGCGAGCAGACGACGCTCTCTGCTGGGCGTTCGAGAAAGACATCTGGTAT 120  
 Qy 121 ATCAAGATGAGCTAAAGCAATGCAAGCATTCCTTAGAGCTGCTGAACATTTATGAAAAG 180  
 Db 121 ATCAAGATGAGCTAAAGCAATGCAAGCATTCCTTAGAGCTGCTGAAGTTATGAAAAG 180  
 Qy 181 AAAGATGAACATAATTAAGGTTTGGCGAGAGCAAAATAGCTGCTGTCTATGACATTGAA 240  
 Db 181 AAAGATGAACATAATTAAGGTTTGGCGAGAGCAAAATAGCTGCTGTCTATGACATTGAA 240  
 Qy 241 GATTCCTCTGATGAATTTAAAGTCCATATTCAGGCGCAAAACCTTATTCCTCAGTTGGTG 300  
 Db 241 GATTCCTCTGATGAATTTAAAGTCCATATTCAGGCGCAAAACCTTATTCCTCAGTTGGTG 300  
 Qy 301 AAATCTCAGAGAACGCCACCGAATTCCTATCCGATTCACAACTTAAATCAAGAGTTGAA 360  
 Db 301 AAATCTCAGAGAACGCCACCGAATTCCTATCCGATTCACAACTTAAATCAAGAGTTGAA 360  
 Qy 361 GAAGTCAGTAGCAGAGAACACACGCTACAGTTTGTAGTCAAGGCTATTCCTCTGGCACAGAG 420  
 Db 361 GAAGTCAGTAGCAGAGAACACACGCTACAGTTTGTAGTCAAGGCTATTCCTCTGGCACAGAG 420  
 Qy 421 ATTGACATCGATTCCTATGAGAGACATTCGTAATCAGTCAGCTCCGCAATTTGGATGAG 480  
 Db 421 GATGACATCGATTCCTATGAGAGACATTCGTAATCAGTCAGCTCCGCAATTTGGATGAG 480  
 Qy 481 GCTGACCTTTGGGTTTTCTGACTCCAAAGAAAAGGCTGCTTGAATATGATCGATACCAAT 540  
 Db 481 GCTGACCTTTGGGTTTTCTGACTCCAAAGAAAAGGCTGCTTGAATATGATCGATACCAAT 540  
 Qy 541 GCTAATGATGGTCCGCGCAAGGTAAATCTGTGTTGTGGGATGGGTGTTAGGCAAGACA 600  
 Db 541 GCTAATGATGGTCCGCGCAAGGTAAATCTGTGTTGTGGGATGGGTGTTAGGCAAGACA 600  
 Qy 601 GCTCTTTCCGAGGAGATCTTTGAAGCGAGAGACATTTAGGAGAACTTCCCTTGCAT 660  
 Db 601 GCTCTTTCCGAGGAGATCTTTGAAGCGAGAGACATTTAGGAGAACTTCCCTTGCAT 660  
 Qy 661 GCTTGGATTCAGTGTCAAAATCATTTTCAAGGATGAGCTACTTAAAGATATGATACGC 720  
 Db 661 GCTTGGATTCAGTGTCAAAATCATTTTCAAGGATGAGCTACTTAAAGATATGATACGC 720  
 Qy 721 CAACCTTCTGGCCCCCAGTCTCTGGATCACTCTTGGCAAGAAATTTGCAAGGAGGTGGTG 780

Db 721 CAACCTCTTGGTCCCAAGTTCTCTGGATCAACTCTTGGATGAATGGCAAGGAAGTGGTG 780  
Qy 781 GTCCAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAGGAGAGAGGTACTTT 840  
Db 781 GTCCAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAGGAGAGAGGTACTTT 840  
Qy 841 GTTGTCTAGATGATCATGTGATTTTACATGATTTGGAATTTGGAATTTGCAATTT 900  
Db 841 GTTGTCTAGATGATCATGTGATTTTACATGATTTGGAATTTGGAATTTGCAATTT 900  
Qy 901 CTTAAGAACATAGAGAGGAGCTCGATAGTAATTAACCACTCGGATGTTGATCTTGG 960  
Db 901 CTTAAGAACATAGAGAGGAGCTCGATAGTAATTAACCACTCGGATGTTGATCTTGG 960  
Qy 961 GAGAAGTGTGCCACAGCTCACTGTGTGTACCACTTGTATTTCTTCCAGATGAACGATGCC 1020  
Db 961 GAGAAGTGTGCCACAGCTCACTGTGTGTACCACTTGTATTTCTTCCAGATGAACGATGCC 1020  
Qy 1021 ATAAATGCTCTAG 1080  
Db 1021 ATTTCAATGCTCTAG 1080  
Qy 1081 ATGCAAAAGATGTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
Db 1081 ATGCAAAAGATGTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
Qy 1141 ACAAATGAGAGCTGTGCTGCAATTAACAGGTGTGAGAGAGAGAGAGAGAGAGAGAG 1200  
Db 1141 ACAAATGAGAGCTGTGCTGCAATTAACAGGTGTGAGAGAGAGAGAGAGAGAGAGAG 1200  
Qy 1201 CTTCTCTCAGAACTAG 1260  
Db 1201 CTTCTCTCAGAACTAG 1260  
Qy 1261 GGTTCACCAACCTACATCCCATTTGAAACCATGCTTTTGTATCTTAAGTATCTTCC 1320  
Db 1261 GGTTCACCAACCTACATCCCATTTGAAACCATGCTTTTGTATCTTAAGTATCTTCC 1320  
Qy 1321 GAGGATTTTGAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
Db 1321 GAGGATTTTGAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
Qy 1381 AGACCAAGTGTGGAG 1440  
Db 1381 AGACCAAGTGTGGAG 1440  
Qy 1441 AACCGAGTATGATTCACAGATCAAGAGTGGGATGAGAGAGAGAGAGAGAGAGAGAG 1500  
Db 1441 AACCGAGTATGATTCACAGATCAAGAGTGGGATGAGAGAGAGAGAGAGAGAGAGAG 1500  
Qy 1501 ATTCAATGATATCCGATGATATCAAGTTCATCTCGAGAGAGAGAGAGAGAGAGAGAG 1560  
Db 1501 ATTCAATGATATCCGATGATATCAAGTTCATCTCGAGAGAGAGAGAGAGAGAGAGAG 1560  
Qy 1561 TTACCAATGGAG 1620  
Db 1561 TTACCAATGGAG 1620  
Qy 1621 GGGAGTATGTCTGCAAAACAGGATTTGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
Db 1621 GGGAGTATGTCTGCAAAACAGGATTTGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
Qy 1681 GGTGACAG 1740  
Db 1681 GGTGACAG 1740  
Qy 1741 GTCTTGGATCTTGAAGATGTGATTTCTTAATCACTCAAAAGAGAGAGAGAGAGAGAG 1800  
Db 1741 GTCTTGGATCTTGAAGATGTGATTTCTTAATCACTCAAAAGAGAGAGAGAGAGAGAG 1800  
Qy 1801 TTGTTGTGCCACTTGAATTTGAGTATTTGATTTGATTTGATTTGATTTGATTTGATTT 1860

Db 1801 TTGTTGTGCCACTTGAATTTGAGTATTTGATTTGATTTGATTTGATTTGATTTGATTT 1860  
Qy 1861 AGATCCATTTGGTAAACTACAGGGCTTCAAACTTTGAACTTGGAGAGAGAGAGAGAGAG 1920  
Db 1861 AGATCCATTTGGTAAACTACAGGGCTTCAAACTTTGAACTTGGAGAGAGAGAGAGAG 1920  
Qy 1921 GCATACCAAGTGTGATCAGTAACTCAATTTCTGATCTCTCTCTCTCTCTCTCTCTCT 1980  
Db 1921 GCATACCAAGTGTGATCAGTAACTCAATTTCTGATCTCTCTCTCTCTCTCTCTCTCT 1980  
Qy 1981 TTTCTATATGACAACTTTTGTCTTAAACCAACCACTTGAAGTGCATATACTAAACAATATGC 2040  
Db 1981 TTTCTATATGACAACTTTTGTCTTAAACCAACCACTTGAAGTGCATATACTAAACAATATGC 2040  
Qy 2041 CTGCTTAAAGTATTTCAACCTTTTGTCTTAAACCACTTGAAGTGCATATACTAAACAATATGC 2100  
Db 2041 CTGCTTAAAGTATTTCAACCTTTTGTCTTAAACCACTTGAAGTGCATATACTAAACAATATGC 2100  
Qy 2101 TTGCACATGGCCACCAAAAGTGTCTGATCTGAAATCAATCGGTGTGAAGGTACCCAAAGGA 2160  
Db 2101 TTGCACATGGCCACCAAAAGTGTCTGATCTGAAATCAATCGGTGTGAAGGTACCCAAAGGA 2160  
Qy 2161 ATAGGTAAAGTGTGCGAGACTTTGCGAGTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220  
Db 2161 ATAGGTAAAGTGTGCGAGACTTTGCGAGTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220  
Qy 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAATTTAGGTGTGACAAACAAC 2280  
Db 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAATTTAGGTGTGACAAACAAC 2280  
Qy 2281 GGGTGCACAAAG 2340  
Db 2281 GGGTGCACAAAG 2340  
Qy 2341 CAATCTCTCAATGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
Db 2341 CAATCTCTCAATGCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
Qy 2401 TCTATTTCT 2460  
Db 2401 TCTATTTCT 2460  
Qy 2461 ATGCTTAACTGGATTTGAGCAGCTCACTCACTGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
Db 2461 ATGCTTAACTGGATTTGAGCAGCTCACTCACTGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
Qy 2521 CTAAAGAGAGGTAAACCACTGCTGATCTTGGGCGAGTGGGCGAGTGGGCGAGTGGGCG 2580  
Db 2521 CTAAAGAGAGGTAAACCACTGCTGATCTTGGGCGAGTGGGCGAGTGGGCGAGTGGGCG 2580  
Qy 2581 CTTTATCGGAATGCTTACCTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640  
Db 2581 CTTTATCGGAATGCTTACCTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640  
Qy 2641 CTTAGAACACTTTTGGATTTTGAATTTGATCAGCTTAAGAGAGAGAGAGAGAGAGAGAG 2700  
Db 2641 CTTAGAACACTTTTGGATTTTGAATTTGATCAGCTTAAGAGAGAGAGAGAGAGAGAGAG 2700  
Qy 2701 AGCTCAGCTCTTGTGGAG 2760  
Db 2701 AGCTCAGCTCTTGTGGAG 2760  
Qy 2761 GGTATCATTTCACTTCCAAAGCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
Db 2761 GGTATCATTTCACTTCCAAAGCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
Qy 2821 GGGCTTTGGTGTGAGGAG 2880  
Db 2821 GGGCTTTGGTGTGAGGAG 2880  
Qy 2881 TACAGTGAACGAG 2940  
Db 2881 TACAGTGAACGAG 2940

QY 2941 CAACAGCAGATCCTGTTCTGTATGTCGCGAGAGATCAGTCACTCTAGCAGTGGAGCAAG 3000  
DB 2941 CAACAGCAGATCCTGTTCTGTATGTCGCGAGAGATCAGTCACTCTAGCAGTGGAGCAAG 3000  
QY 3001 GATCCCTTCCCGAGCAGGAGGAGAGAGCTCGCAGTGCAGGTGATCAAGTTGAGCAGC 3060  
DB 3001 GATCCCTTCCCGAGCAGGAGGAGAGAGCTCGCAGTGCAGGTGATCAAGTTGAGCAGC 3060  
QY 3061 AATGATAGCAAGAGATAGGCACAGCTCAAGTGGCTCA 3099  
DB 3061 AATGATAGCAAGAGATAGGCACAGCTCAAGTGGCTCA 3099

## RESULT 5

US-10-656-394A-16

; Sequence 16, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; FILE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035718/252062

; CURRENT APPLICATION NUMBER: US/10/656,394A

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 3674

; TYPE: DNA

; ORGANISM: Oriza minuta

US-10-656-394A-16

Query Match 93.9%; Score 2910.2; DB 8; Length 3674;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 1 ATGCGGAGAGCGTGTGAGCATGGCGAGTGGCTGCTGGTGGGCGAGCGCCATCAGCAAGGCC 60  
DB 9 ATGCGGAGAGCGTGTGAGCATGGCGAGTGGCTGCTGGTGGGCGAGCGCCATCAGCAAGGCC 68  
QY 61 GCCTCCGCTGTCGCGAGCAGACAGCCCTCTGCTGGGCGTGGCGAGAAAGACATCTGTAT 120  
DB 69 GCCTCTCCGCTGCGAATGAGCAGCAGCCCTCTGCTGGGCGTGGCGAGAAAGACATCTGTAT 128  
QY 121 ATCAAGATGAGCTTAAAGCGATGCAAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG 180  
DB 129 ATCAAGATGAGCTTAAAGCGATGCAAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG 188  
QY 181 AAAGATGAACTTAAAGGTTGGGCGAGAGCAAAATAGCTGACCTGTCTATGACATTTGAA 240  
DB 189 AAAGATGAACTTAAAGGTTGGGCGAGAGCAAAATAGCTGACCTGTCTATGACATTTGAA 248  
QY 241 GATTCCTTGAATTAAGTTCATATTTAAAGCCTTAAAGCCTTAAAGCCTTAAAGCCTTAAAG 300  
DB 249 GATTCCTTGAATTAAGTTCATATTTAAAGCCTTAAAGCCTTAAAGCCTTAAAGCCTTAAAG 308  
QY 301 AAATCTAGAGAACCCCAAGTTGCTATCGTATTCACACCTTAAATCAAGGTTGAA 360  
DB 309 AAATCTAGAGAACCCCAAGTTGCTATCGTATTCACACCTTAAATCAAGGTTGAA 368  
QY 361 GAAGTGAAGTGAAGGACACAGCTACAGTTAGTCAAGCTTATTCCTCTGGCAGCAGAG 420  
DB 369 GAAGTGAAGTGAAGGACACAGCTACAGTTAGTCAAGCTTATTCCTCTGGCAGCAGAG 428  
QY 421 ATTGACATGATTCCTATGAGAGACATTCGTAATCAAGTCAAGCTTCAAGTCAAGTCAAG 480  
DB 429 GATGACATGATTCCTATGAGAGACATTCGTAATCAAGTCAAGCTTCAAGTCAAGTCAAG 488  
QY 481 GCTGAGCTGTTGGTCTTCTGACTCCAGAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
DB 489 GCTGAGCTGTTGGTCTTCTGACTCCAGAGAAAGGCTGCTTGAATGATCGATACCAAT 548

QY 541 GCTAATGATGTCGCGCAAGGTAACTGTGTGTGGATGGGTGGTGTAGGCAAGACA 600  
DB 549 GCTAATGATGTCGCGCAAGGTAACTGTGTGTGGATGGGTGGTGTAGGCAAGACA 608  
QY 601 GCTCTTTTCAGGAAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660  
DB 609 GCTCTTTTCAGGAAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 668  
QY 661 GCTTGGATTTACAGTGTCAACATCACTTCAAGGATTCAGCTTCTTAAAGATATGATACGC 720  
DB 669 GCTTGGATTTACAGTGTCAACATCACTTCAAGGATTCAGCTTCTTAAAGATATGATACGC 728  
QY 721 CAACCTTTCTGGCCCGAGTTCTCTGATCACTCTTTCAGAAATTTGCAAGGAGAGTGGTG 780  
DB 729 CAACCTTTCTGGCCCGAGTTCTCTGATCACTCTTTCAGAAATTTGCAAGGAGAGTGGTG 788  
QY 781 GTGCAAGTACATCATCTTTCTGAGTACCTCTAGATAGAGCTCAAGGAGAGAGAGTACTTT 840  
DB 789 GTGCAAGTACATCATCTTTCTGAGTACCTCTAGATAGAGCTCAAGGAGAGAGAGTACTTT 848  
QY 841 GTTGTCTTAGATGATCTATGATTTTACATGATTTGGAATTTGGATTAATGAAATTTGCATTT 900  
DB 849 GTTGTCTTAGATGATCTATGATTTTACATGATTTGGAATTTGGATTAATGAAATTTGCATTT 908  
QY 901 CCTAAGACAATAAGAGAGGCGAGTCAATAGTAACTCACTCGGAATTTGATCTTGGC 960  
DB 909 CCTAAGACAATAAGAGAGGCGAGTCAATAGTAACTCACTCGGAATTTGATCTTGGC 968  
QY 961 GAGAAGTGTGCCACAGCCCTCACTGTGTACCACTTGAATTTCTTTCAGAGATGAAGATGCC 1020  
DB 969 GAGAAGTGTGCCACAGCCCTCACTGTGTACCACTTGAATTTCTTTCAGAGATGAAGATGCC 1028  
QY 1021 ATAACTTCTGCTACTGAGAAACAAATAAAATCATGAAGACATGGAATCAATATAAAAT 1080  
DB 1029 ATAACTTCTGCTACTGAGAAACAAATAAAATCATGAAGACATGGAATCAATATAAAAT 1088  
QY 1081 ATCAAAAGATGTTGAAAGCAATTTAAATTAATTTGCTGTCTTACCATTTAGCAATACTT 1140  
DB 1089 ATCAAAAGATGTTGAAAGCAATTTAAATTAATTTGCTGTCTTACCATTTAGCAATACTT 1148  
QY 1141 ACATAGGAGCTGTCTGCACTAAACAGAGTGTGAGATGGGAGAAATTTCTATGAACAC 1200  
DB 1149 ACATAGGAGCTGTCTGCACTAAACAGAGTGTGAGATGGGAGAAATTTCTATGAACAC 1208  
QY 1201 CTTCTTCAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGAAATTTGAGACCCCTA 1260  
DB 1209 CTTCTTCAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGAAATTTGAGACCCCTA 1268  
QY 1261 GGTTCAGAACCCCTACCTCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTTCCCT 1320  
DB 1269 GGTTCAGAACCCCTACCTCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTTCCCT 1328  
QY 1321 GAGGATTTGAAATCAAAAGGAATCGTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTGT 1380  
DB 1329 GAGGATTTGAAATCAAAAGGAATCGTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTGT 1388  
QY 1381 AGACCAAGTGTGGATGACAGTAAAGATGTCGAGAGAACTTACTTTAATGAGCTAATC 1440  
DB 1389 AGACCAAGTGTGGATGACAGTAAAGATGTCGAGAGAACTTACTTTAATGAGCTAATC 1448  
QY 1441 AACCGAAGTATGATTTCAACGATCAAGAGTGGGCAATGAGGAGAAATTTAAGACTTGTGCA 1500  
DB 1449 AACCGAAGTATGATTTCAACGATCAAGAGTGGGCAATGAGGAGAAATTTAAGACTTGTGCA 1508  
QY 1501 ATTATGATATCATCGGTGATATCAGTTTCACTCTGAGACAGGAGAAATTTTGTATTA 1560  
DB 1509 ATTATGATATCATCGGTGATATCAGTTTCACTCTGAGACAGGAGAAATTTTGTATTA 1568  
QY 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAGAAACACTCGCCCAATAGCAATTCAT 1620  
DB 1569 TTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAGAAACACTCGCCCAATAGCAATTCAT 1628  
QY 1621 GGGAGTATGTCCTGCAAAACTGGATTTGGATTTGAGCATTTATTCGATCATTTAGCTATTTT 1680









QY 2577 TCATCTTTATCGGAATGCTTACCTTGGGAGAGAGCTAGTATTCAAAAACAGGAGCAATCCC 2636  
DB 2754 TTATCTTTATGGAAATGCTTACCTTGGGAGAGAGCTAGTATTCAAAACGGGAGCAATCCC 2813  
QY 2637 AAATCTTGAACACTTCTGGATTTATGAATGATCGCTTAAGAGAGATCAGATTTGAGA 2696  
DB 2814 AAATCTTGAACACTTCTGGATTTATGAATGATCGCTTAAGAGAGATCAGATTTGAGA 2873  
QY 2697 CGGCAGCTCAACCCCTGTTGGAAAGATAGAAATAGCGGAGTGCAGGTTCGAATCTGGAT 2756  
DB 2874 TGGCAGCTCAACCCCTGTTGGAAAGATAGAAATCTTCTGCTGCAGGTTCGAATCAGGAT 2933  
QY 2757 TACTGGATCAATTCACCTTCCAAAGCTCAAGAGATTCGAATTAAGATCAGGAGTAAAGT 2816  
DB 2934 TATTGGATCAATTCACCTTCCAAAGCTCAAGAGATTCGAATTAAGATCAGGAGTAAAGT 2993  
QY 2817 GGCTGGCTTGGTCACTGAGGAGAGAGTGAACGACACCAATCGCCCGTGTCTGCT 2876  
DB 2994 GGCTAGCTTGGTCACTGAGGAGAGAGTGAACGACACCAATCGCCCGTGTCTGCT 3053  
QY 2877 AATGTACAGTGAACGAAGTATCAAGCTGGGGCTGAGCGGAGAGATCTCTATAGA 2936  
DB 3054 AATGTACAGTGAACGAAGTATCAAGCTGGGGCTGAGCGGAGAGATCTCTATAGA 3113  
QY 2937 AGTCAACAGCAGATCTCTGCTGATGCGGAGAGAGTCACTGAGCAGTGAAGC 2996  
DB 3114 AGTCAACAGCAGATCTCTGCTGATGCGGAGAGAGTCACTGAGCAGTGAAGC 3173  
QY 2997 AACGGATCCCTTCCCGAGCAGGAGGAGAGTCCGAGTCCGAGTGAAGC 3056  
DB 3174 AACGGATCCCTTCCCGAGCAGGAGGAGAGTCCGAGTCCGAGTGAAGC 3233  
QY 3057 GACGAATGATAGCAGAGATAGGACAGCTCAAGCTGGCTGA 3099  
DB 3234 GACGAATGATAGCAGAGATAGGACAGCTCAAGCTGGCTGA 3276

RESULT 7

US-10-352-179-83  
; Sequence 83, Application US/10352179  
; Publication No. US20040006788A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Guo-liang  
; APPLICANT: Liu, Guifu  
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla  
; FILE REFERENCE: 22727/04108  
; CURRENT APPLICATION NUMBER: US/10/352,179  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/352,106  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 76272  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
US-10-352-179-83

Query Match 91.0%; Score 2820.4; DB 6; Length 76272;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 2872; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
QY 116 GGTATATCAAGATGAGCTAAACGATGCAAGCATTCCTTAGAGCTGCTGAACCTATGA 175  
DB 62061 GGTATATCAAGATGAGCTAAACGATGCAAGCATTCCTTAGAGCTGCTGAACCTATGA 62120  
QY 176 AAAAGAAAGATGAATTAATTAAGGTTTGGGAGAGCAATACGTCATGATGACA 235  
DB 62121 AAAAGAAAGATGAATTAATTAAGGTTTGGGAGAGCAATACGTCATGATGACA 62180  
QY 236 TTGAAGATCCCTTGATGAATTTAAGTCCATTTGAAGCCAAACCTATTTCGTGAGT 295

DB 62181 TTGAAGATCCCTTGATGAATTTAAGTCCATTTGAAGCCAAACCTATTTCGTGAGT 62240  
QY 296 TGGTGAACACTCAGAGAAACGCGACCGAATTTGCTATCCGTATCCCAACCTTTAAATCAAGAG 355  
DB 62241 TGGTGAACACTCAGAGAAACGCGACCGAATTTGCTATCCGTATCCCAACCTTTAAATCAAGAG 62300  
QY 356 TTGAAGAACTGAGTACAGGAAACACGCTACAGTTTGTAGTCAAGCCCTATTTCCTCTGGCA 415  
DB 62301 TTGAAGAACTGAGTACAGGAAACACGCTACAGTTTGTAGTCAAGCCCTATTTCCTCTGGCA 62360  
QY 416 CAGAGATTCACATGATTTCTTATGCAAGAGCAATTCGTATCAAGTCAAGTTCGCAATGTGG 475  
DB 62361 CAGAGATTCACATGATTTCTTATGCAAGAGCAATTCGTATCAAGTCAAGTTCGCAATGTGG 62420  
QY 476 ATGAGCTGAGCTTCTTGGGTTTCTGACTCCAGAAAGCTGCTGAAATCATGATGATA 535  
DB 62421 ATGAGCTGAGCTTCTTGGGTTTCTGACTCCAGAAAGCTGCTGAAATCATGATGATA 62480  
QY 536 CCAATGCTAATGATGCTCGGCGCAAGGTAATCTGTGTTGCGATGGGTGGTTAGGCA 595  
DB 62481 CCAATGCTAATGATGCTCGGCGCAAGGTAATCTGTGTTGCGATGGGTGGTTAGGCA 62540  
QY 596 AGACAGCTCTTTTGGAGAGATCTTTGAAAGCGAAGAGCAATTTAGCAAGAACTTCCCTT 655  
DB 62541 AGACAGCTCTTTTGGAGAGATCTTTGAAAGCGAAGAGCAATTTAGCAAGAACTTCCCTT 62600  
QY 656 GCAATGCTTGGATTTACAGTGTCACAATCATTTTCAAGGATTTGAGTCTTTAAAGATATGA 715  
DB 62601 GCAATGCTTGGATTTACAGTGTCACAATCATTTTCAAGGATTTGAGTCTTTAAAGATATGA 62660  
QY 716 TAGCCCAACTTTTGGCCCCAGTCTCTGAGTCAACTCTTTCGAAGAACTTTGCAAGGAGAG 775  
DB 62661 TAGCCCAACTTTTGGCCCCAGTCTCTGAGTCAACTCTTTCGAAGAACTTTGCAAGGAGAG 62720  
QY 776 TGGTGGTCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGAGAGAGAGGT 835  
DB 62721 TGGTGGTCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGAGAGAGAGGT 62780  
QY 836 ACTTTGCTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 895  
DB 62781 ACTTTGCTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 62840  
QY 896 CATTTCTTAAGAACCAATTAAGAGGAGCTCGAATTAATTAACCACTTCGGAATTTGATC 955  
DB 62841 CATTTCTTAAGAACCAATTAAGAGGAGCTCGAATTAATTAACCACTTCGGAATTTGATC 62900  
QY 956 TTCCGGAGAGTGTGCCACAGCTCCTCACTGGTGTACCACTTGTATTTCTTCAGATGAGC 1015  
DB 62901 TAGCCGAGAGAGTGTGCCACAGCTCCTCACTGGTGTACCACTTGTATTTCTTCAGATGAGC 62960  
QY 1016 ATGCCATACATTTGCTTACTTGAGAAACCAATTAATTAATTAATTAATTAATTAATTAAT 1075  
DB 62961 ATGCCATACATTTGCTTACTTGAGAAACCAATTAATTAATTAATTAATTAATTAATTAAT 63020  
QY 1076 AAAATATGCAAAAGATGTTGAACGAATTTGTAATTAATTAATTAATTAATTAATTAATTAAT 1135  
DB 63021 AAAATATGCAAAAGATGTTGAACGAATTTGTAATTAATTAATTAATTAATTAATTAATTAAT 63080  
QY 1136 TACTTCAATAGAGCTGTGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1195  
DB 63081 TACTTCAATAGAGCTGTGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 63140  
QY 1196 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTTCAGAGAGATGTTGA 1255  
DB 63141 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTTCAGAGAGATGTTGA 63200  
QY 1256 CCCTAGGTTCACCACTTACCTCCCACTTTGAAACCACTGCTTTTCTTCTTCTTCTTCTTCTTCT 1315  
DB 63201 CCCTAGGTTCACCACTTACCTCCCACTTTGAAACCACTGCTTTTCTTCTTCTTCTTCTTCTTCT 63260  
QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGATGATGATGATGATGATGAT 1375  
DB 63261 TTCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGATGATGATGATGATGATGAT 63320

QY 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGC 1435  
DB 63321 TTGTTAGACCGCAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGC 63380  
QY 1436 TAATCAACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAATTAAGACTT 1495  
DB 63381 TAATCAGCGGAAGTATGATTCACAGATCAAGAGTGGGCATATCAGGAAATTAAGACTT 63440  
QY 1496 GTCGAATTCATGATATCATCCGTTGATATCACAGTTTCATCTCCGAGCAGGAAATTTTG 1555  
DB 63441 GTCGAATTCATGATATCATCCGTTGATATCACAGTTTCATCTCCGAGCAGGAAATTTTG 63500  
QY 1556 TATTATTACCAATGGGAGATGGCTCTGATTTAGTTTACGAGAAACACCTGCCACATAGCAT 1615  
DB 63501 TATTGTTACCAATGGGAGATGGCTCTGATTTAGTTTACGAGAAACACCTGCCACATAGCAT 63560  
QY 1616 TCCATGGGAGTATGTCCTGCAAACTGGATTTGGATGGAGCAATTTATTCGATCATTAGCTA 1675  
DB 63561 TCCATGGGAGTATGTCCTGCAAACTGGATTTGGATGGAGCAATTTATTCGATCATTAGCTA 63620  
QY 1676 TTTTGTGTGACAGACCCCAAGAGTCTAGCACATGCGAGTTTGTCCAGATCAATTTGAGGATG 1735  
DB 63621 TTTTGTGTGACAGACCCCAAGAGTCTAGCACATGCGAGTTTGTCCAGATCAATTTGAGGATG 63680  
QY 1736 TACGGGCTTGGATTTGGAAGATGTGACATTTCTTAATCACTCAAAAGATTTGACCGTA 1795  
DB 63681 TACGGGCTTGGATTTGGAAGATGTGACATTTCTTAATCACTCAAAAGATTTGACCGTA 63740  
QY 1796 TTGCATTTGTTGTGCCACTTGAATATCTTGAGTATTTGGATATTCGTCATCCATATATTCAC 1855  
DB 63741 TTGCATTTGTTGTGCCACTTGAATATCTTGAGTATTTGGATATTCGTCATCCATATATTCAC 63800  
QY 1856 TTCCAGATTCATTTGTAATCTACAGGCTTCAAACTTTGACATCGGAGCATACA 1915  
DB 63801 TTCCAGATTCATTTGTAATCTACAGGCTTCAAACTTTGACATCGGAGCATACA 63860  
QY 1916 TTGCAGCACTACCAAGTGAGATCAGTAAACTTCAATGTCTGATATCTTCTGTTGATAG 1975  
DB 63861 TTGCAGCACTACCAAGTGAGATCAGTAAACTTCAATGTCTGATATCTTCTGTTGATAG 63920  
QY 1976 GACAGTTTCATTTAGACATTTTAGTCTTAAACCCCAATGAGTGATTAATCAACAA 2035  
DB 63921 GAAAGTTTGTGTTATGACAACTTTAGTCTTAAACCCCAATGAGTGATTAATCAACAA 63980  
QY 2036 TATGCTGCTTAAAGTATTCACACCTTTAGTTAGTTCGGATGATCGTCAAAACAAATTTG 2095  
DB 63981 TATGCTGCTTAAAGTATTCACACCTTTAGTTAGTTCGGATGATCGTCAAAACAAATTTG 64040  
QY 2096 CTGAATTTGCATGCGCACCAAAAGTTGCTGTGATCAATCGGTGAGGTACCCA 2155  
DB 64041 CTGAATTTGCATGCGCACCAAAAGTTGCTGTGATCAATCGGTGAGGTACCCA 64100  
QY 2156 AAGGAATAGGTAAGTTCGGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCA 2215  
DB 64101 AAGGAATAGGTAAGTTCGGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCA 64160  
QY 2216 GTAGTAGGCAATCAAGAGCTGGGCGAGTTAAGCAGTTCGAGGAAATTAGGTGTGACAA 2275  
DB 64161 GTAGTAGGCAATCAAGAGCTGGGCGAGTTAAGCAGTTCGAGGAAATTAGGTGTGATNA 64220  
QY 2276 CAACCGGCTGCACAAAGGAAATTTAAGATCTTTATGACCCATTCGAGAGCTCTCTT 2335  
DB 64221 CAACCGGCTGCACAAAGGAAATTTAAGATCTTTATGACCCATTCGAGAGCTCTCTT 64280  
QY 2336 CCTTCCATCTCTCCATGTGGATGTCGAGGAATCTCAGATGGTGGAACTCTGAGTGCC 2395  
DB 64281 CCTTCCATCTCTCTATGTGAATGCTCGGTTATATCAGATTTGAAACACTTCGAGTGCC 64340  
QY 2396 TAGATTCTATTTCATCT 2455  
DB 64341 TAGATTCTATTTCATCT 64400

QY 2456 AGCAGATGCTTAATCGGATTGAGCAGCTCACTCACCTCGAAGAGATCTACTTATTGAGGA 2515  
DB 64401 AAGGATGCTTAATCGGATTGAGCAGCTCACTCACCTCGAAGAGATCTACTTATTGAGGA 64460  
QY 2516 GCAAACTAAAGGAAGGTAACCATGCTGATACCTTTGGGGCACTGCCCACTCATGCTCC 2575  
DB 64461 GCAAACTAAAGGAAGGTAACCATGCTGATACCTTTGGGGCACTTTGCCCACTCATGCTCC 64520  
QY 2576 TTTCTTTTATCGGAATGCTTACCTTTGGGGAAGAGTAGTATTCAAAAACAGGAGCATTTCC 2635  
DB 64521 TTTCTTTTATCGGAATGCTTACCTTTGGGGAAGAGTAGTATTCAAAAACAGGAGCATTTCC 64580  
QY 2636 CAAATCTTAGAACACCTTTTGGATTTAGATTTGGATTCAGCTCAAGAGATCAGATTTGAGG 2695  
DB 64581 CAAATCTTAGAACACCTTTTGGATTTAGATTTGGATTCAGCTCAAGAGATCAGATTTGAGG 64640  
QY 2696 ACCGAGCTCACCCCTTTGGAAAGATAGAAATAGGCGAGTGCAGGTTTGAATCTGGGA 2755  
DB 64641 ATGGCAGCTCACCCCTTTGGAAAGATAGAAATCTCTTGTCTGCAGGTTGGAATCAGGA 64700  
QY 2756 TTAATCTGATATCATCTTCCAAAGCTCAAGGAGATTTCCAAATTTAGATACGGAAGTAAAG 2815  
DB 64701 TTAATCTGATATCATCTTCCAAAGCTCAAGGAGATTTCCAAATTTAGATACGGAAGTAAAG 64760  
QY 2816 TGCTCGGCTTGTGTCAGCTGAGGAGGAGAGTGAACGACACCCAAATCGCCCTGCTGC 2875  
DB 64761 TGCTCGGCTTGTGTCAGCTGAGGAGGAGAGTGAACGACACCCAAATCGCCCTGCTGC 64820  
QY 2876 TAAATGATGATGACGGAAGTATACGACCTTGGGGGCTGAAGCGAAGGATCTTCTATAG 2935  
DB 64821 GAATGACAGTGTACCGAAGGATTCAGACCTTGGGGGCTGAAGCGAAGGATCTTCTATAG 64880  
QY 2936 AAGTGCAAAACAGCAGATCTCTGATGCGGAGAGATCAGTCACTGTAGCAGTGAAG 2995  
DB 64881 AAGTGCAAAACAGCAGATCTCTGATGCGGAGAGATCAGTCACTGTAGCAGTGAAG 64940  
QY 2996 CAACGATCCCTTCCGAGCAGGAGGAGAGCTGCGAGTCCGAGGTGATCAGCTTGA 3055  
DB 64941 CAACGATCCCTTCCGAGCAGGAGGAGAGCTGCGAGTCCGAGGTGATCAGCTTGA 65000  
QY 3056 CGACGATGATAGCGAAG 3073  
DB 65001 CGACGATGATAGGTGAG 65018

## RESULT 8

US-10-437-963-37316

; Sequence 37316, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 37316

; LENGTH: 4596

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_41056C.1

US-10-437-963-37316

Query Match

82.8%; Score 2565.2; DB 7; Length 4596;

Best Local Similarity 98.3%; Pred. No. 0; Matches 2604; Conservative 0; Mismatches 43; Indels 3; Gaps 1;			
Qy	422	TTGACATGATTCCTATGAGAGACATTCGTAATCAGTCAGCTCGCAATGTCGATGAGG	481
Ds	29	TAGCAATAGATTCCTATGAGAGACATTCGTAATCAGTCAGCTCGCAATGTCGATGAGG	88
Qy	482	CTGAGCTGTGTGGGTTTCTGATCTCAAGAAAGGCTGCTGAAATGATCGATACCAATG	541
Ds	89	CTGAGCTGTGTGGGTTTCTGATCTCAAGAAAGGCTGCTGAAATGATCGATACCAATG	148
Qy	542	CTAATGATGTCCGCGCAAGGTAATCTGTGTGTGGATGGGTGTTTGGGCAAGACAG	601
Ds	149	CTAATGATGTCCGCGCAAGGTAATCTGTGTGTGGATGGGTGTTTGGGCAAGACAG	208
Qy	602	CTCTTTGAGGAAGATCTTTGAAAGCAAGAGACATTTAGGAAGAACTTCCCTTGGCAATG	661
Ds	209	CTCTTTGAGGAAGATCTTTGAAAGCAAGAGACATTTAGGAAGAACTTCCCTTGGCAATG	268
Qy	662	CTTGGATCAGGTGCACATCATTTCAAGGATGAGTACTTAAAGATATGATAGCC	721
Ds	269	CTTGGATCAGGTGCACATCATTTCAAGGATGAGTACTTAAAGATATGATAGCC	328
Qy	722	AACCTTTGCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCAGAGGAAGGTGGTG	781
Ds	329	AACCTTTGCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCAGAGGAAGGTGGTG	388
Qy	782	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGTACTTTG	841
Ds	389	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGTACTTTG	448
Qy	842	TTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATTTGAAATTTGCAATTC	901
Ds	449	TTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATTTGAAATTTGCAATTC	508
Qy	902	CTAAGAAACAATAAGAGGAGTCTGATATGATTAACCACTCGGAATTTGATCTGCGG	961
Ds	509	CTAAGAAACAATAAGAGGAGTCTAATAATGATTAACCACTCGGAATTTGATCTGCGG	568
Qy	962	AGAGTGTGCAAGGCTCACTGTGTGACACCTTGTATTTCTTGCAGATGAAGATGCCA	1021
Ds	569	AGAGTGTGCAAGGCTCACTGTGTGACACCTTGTATTTCTTGCAGATGAAGATGCCA	628
Qy	1022	TAACTTGTCTAGAGAAACAATAATAAATCATGAAGACATGGAATCAATAAATA	1081
Ds	629	TAACTTGTCTAGAGAAACAATAATAAATCATGAAGACATGGAATCAATAAATA	688
Qy	1082	TGCAAAAGATGGTTGAACGAATTTGTAATAATGTTGCTCTACCAATTAAGCAATCTTA	1141
Ds	689	TGCAAAAGATGGTTGAACGAATTTGTAATAATGTTGCTCTACCAATTAAGCAATCTTA	748
Qy	1142	CAATAGAGCTGTCTTGCATCAATCAAGGTCTCAAGATGGGAGAAATTTATGAACACC	1201
Ds	749	CAATAGAGCTGTCTTGCATCAATCAAGGTCTCAAGATGGGAGAAATTTATGAACACC	808
Qy	1202	TTCCCTTCAAGACTAGAAATAAACCCAGGCTCGAAGCTTTGAGGAGATGTCACCTAG	1261
Ds	809	TTCCCTTCAAGACTAGAAATAAACCCAGGCTCGAAGCTTTGAGGAGATGTCACCTAG	868
Qy	1262	GTTACACACCACTACCATCCCAATTTGAAACCAATGCTTTTGTATCTAAGTATCTTCTTG	1321
Ds	869	GTTACACACCACTACCATCCCAATTTGAAACCAATGCTTTTGTATCTAAGTATCTTCTTG	928
Qy	1322	AGGATTTTGAATCAAGGAATCGTCTAGTAGTAGTATGATGATGAGAGAGGTTTGTTA	1381
Ds	929	AGGATTTTGAATCAAGGAATCGTCTAGTAGTAGTATGATGATGAGAGAGGTTTGTTA	988
Qy	1382	GACCAAGGTTGGGATGACGACTTAAGGATGTCGAGAGAAATTTCTTAATGAGCTATCA	1441
Ds	989	GACCAAGGTTGGGATGACGACTTAAGGATGTCGAGAGAAATTTCTTAATGAGCTATCA	1048
Qy	1442	ACCAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAATTAAGACTTGTGCA	1501

Ds	1049	ACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGCA	1108
Qy	1502	TTCATGATATCATCGTGTATATCAAGTTTCAATCTCGACAGAGAAAAATTTTGTATTAT	1561
Ds	1109	TTCATGATATCATCGTGTATATCAAGTTTCAATCTCGACAGAGAAAAATTTTGTATTAT	1168
Qy	1562	TACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAAACATCGCCACATAGCATTCATG	1621
Ds	1169	TACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAAACATCGCCACATAGCATTCATG	1228
Qy	1622	GGAGTATGCTTCGCAAAAATCGAATGGATGGAGCATTTTCGATCATTAAGCTATTTTTG	1681
Ds	1229	GGAGTATGCTTCGCAAAAATCGAATGGATGGAGCATTTTCGATCATTAAGCTATTTTTG	1288
Qy	1682	GTGACAGACCCAGAGTCTAGCAGATGCTGTCAGATTTGTCAGATCAATTGAGGATGTTACGGG	1741
Ds	1289	GTGACAGACCCAGAGTCTAGCAGATGCTGTCAGATTTGTCAGATCAATTGAGGATGTTACGGG	1348
Qy	1742	TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCAAT	1801
Ds	1349	TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCATATTGCAAT	1408
Qy	1802	TGTTGTGCCATCTTGAATTAATCTTGTGATTTGATTTGTCATCTCATATATTTCCTTCCCA	1861
Ds	1409	TGTTGTGCCATCTTGAATTAATCTTGTGATTTGTCATCTCATATATTTCCTTCCCA	1468
Qy	1862	GATCCATTTGGTAAAATCTACAGGCGCTCAAAAATTTTGAACATGCGGAGCACATATGCGAG	1921
Ds	1469	GATCCATTTGGTAAAATCTACAGGCGCTCAAAAATTTTGAACATGCGGAGCACATATGCGAG	1528
Qy	1922	CACATCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1981
Ds	1529	CACATCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1588
Qy	1982	TTCAATTTACCAAACTTTTGTCTTAAACCAACCACTTAAAGTGCATTAACCAATATGCC	2041
Ds	1589	TTCAATTTACCAAACTTTTGTCTTAAACCAACCACTTAAAGTGCATTAACCAATATGCC	1648
Qy	2042	TGCTTAAAGTATTCACATCTTTAGTTCGCGATGATGATGATGATGATGATGATGATGATGAT	2101
Ds	1649	TGCTTAAAGTATTCACATCTTTAGTTCGCGATGATGATGATGATGATGATGATGATGATGAT	1708
Qy	2102	TGCACATGCGCAACCAAGTTGCTGCTGATCAATCAATCGGTGTGAAGTACCCAAAGGAA	2161
Ds	1709	TGCACATGCGCAACCAAGTTGCTGCTGATCAATCAATCGGTGTGAAGTACCCAAAGGAA	1768
Qy	2162	TAGGTAAGTTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2221
Ds	1769	TAGGTAAGTTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1828
Qy	2222	GAGCAATCAAGAGCTGGGCGAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGACCAACAAACG	2281
Ds	1829	GAGCAATCAAGAGCTGGGCGAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGACCAACAAACG	1888
Qy	2282	GGTTCGCAAGGAAAGAAATGTAAGATACCTTTTATGAGCACTTTGAGAACTCTTCTCCCTCC	2341
Ds	1889	GGTTCGCAAGGAAAGAAATGTAAGATACCTTTTATGAGCACTTTGAGAACTCTTCTCCCTCC	1948
Qy	2342	AATCTCTCAATGTGATGCTGAGGATCTCAG--ATGTTGGAACACTTGTGATGCTAG	2398
Ds	1949	AATCTCTCAATGTGATGCTGAGGATCTCAG--ATGTTGGAACACTTGTGATGCTAG	2008
Qy	2399	ATTCTATTCT	2458
Ds	2009	ATTCTATTCT	2068
Qy	2459	AGATGCTTAATCTGATGAGGATCTCTACCTGAGAGAGATCTACTATTTCAGGAGCA	2518
Ds	2069	AGATGCTTAATCTGATGAGGATCTCTACCTGAGAGAGATCTACTATTTCAGGAGAGCA	2128
Qy	2519	AACCTAAGGAAAGTAAACCAATGCTGATACCTTGGGCACTGCGCCCAACCTCATGCTCTTC	2578
Ds	2129	AACCTAAGGAAAGTAAACCAATGCTGATACCTTGGGCACTGCGCCCAACCTCATGCTCTTC	2188

QY 2579 ATCTTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTCAAACAGGAGCATTCCTCAA 2638  
DB 2189 ATCTTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTCAAACAGGAGCATTCCTCAA 2248  
QY 2639 ATCTTAGAACACATTTGGATTATGAATTTGGATTCAGCTAAGAGAGATCAGATTGGAGAGC 2698  
DB 2249 ATCTTAGAACACATTTGGATTATGAATTTGGATTCAGCTAAGAGAGATCAGATTGGAGAGC 2308  
QY 2699 GCAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGATCTGGGATTA 2758  
DB 2309 GCAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGATCTGGGATTA 2368  
QY 2759 CTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACGGAAGTAAAGTGG 2818  
DB 2369 TTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACGGAAGTAAAGTGG 2428  
QY 2819 CTGGGCTTGGTTCAGCTGGAGGAGAGTGAACGACACCCCAATTCGCCCTGCTGCTAA 2878  
DB 2429 CTGGGCTTGGTTCAGCTGGAGGAGAGTGAACACACACCCCAATTCGCCCTGCTGCTAA 2488  
QY 2879 TGTAAGTGCACCAAGGTATCACGACCTGGGGGCTGAAGCCGAGGATCTTCTATAGAAG 2938  
DB 2489 TGTAAGTGCACCAAGGTATCACGACCTGGGGGCTGAAGCCGAGGATCTTCTATAGAAG 2548  
QY 2939 TGCAACAGCAGATTCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGCAA 2998  
DB 2549 TGCAACAGCAGATTCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGCAA 2608  
QY 2999 CGGATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGCATCACTGTAGCAGTGGAGCAA 3058  
DB 2609 CGGATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGCATCACTGTAGCAGTGGAGCAA 2668  
QY 3059 CGAATGATAG 3068  
DB 2669 CGAATGATAG 2678

## RESULT 9

US-10-656-394A-11  
; Sequence 11, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE REFERENCE: broad-spectrum resistance gene p12  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 2997  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2997)  
US-10-656-394A-11

Query Match 77.2%; Score 2393.6; DB 8; Length 2997;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 2453; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
QY 422 TTGACATGATTCCTATGCGAAGACATTCGTAATCAGTCCGCAATGTGGATGAGG 481  
DB 197 TAGCAATAGATTCCTATGCGAAGACATTCGCAATCAATCAGCTCGAATGTGGATGAGG 256  
QY 482 CTGAGCTGTGTGGGTTTCTGACTCCAGAAAGGCTGCTGAAATGATCGATACCAATG 541  
DB 257 CTGAGCTGTGTGGGTTTCTGACTCCAGAAAGGCTGCTGAAATGATCGATACCAATG 316  
QY 542 CTAATGATGTCGGCCCAAGGTAAATCTGTGTTGGGATGGGTGTTAGGCGAAGACAG 601

DB 317 CTANTGATGTCGGCCCAAGGTAAATCTGTGTTGGATGGGTGTTTAGGCAAGACAG 376  
QY 602 CTCTTTGCGAGAGATCTTTGAAAGCGAGAGACATTTAGGAAGAACTTCCCTTGCATG 661  
DB 377 CTCTTTGCGAGAGATCTTTGAAAGCGAGAGACATTTAGGAAGAACTTCCCTTGCATG 436  
QY 662 CTGGAATACAGTGTCAACATCATTTACAGGATTTGAGCTACTTAAAGATATGATACGCC 721  
DB 437 CTGGAATACAGTGTCAACATCATTTACAGGATTTGAGCTACTTAAAGATATGATACGCC 496  
QY 722 AACTTCTTGCCGCCAGTCTCTGGAATCAACTCTTTCGAAGAATTCGAAGGAGAGTGGTGG 781  
DB 497 AACTTCTTGCCGCCAGTCTCTGGAATCAACTCTTTCGAAGAATTCGAAGGAGAGTGGTGG 556  
QY 782 TGCAGATCATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGATCTTTG 841  
DB 557 TGCAGATCATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGATCTTTG 616  
QY 842 TTGTTCTAGATCATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGCAATTTTC 901  
DB 617 TTGTTCTAGATCATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGCAATTTTC 676  
QY 902 CTAAGAAACAATAAGAGGCGCAGTTCGAATAGTAAACACCTCGGAATTTGATCTTGGCG 961  
DB 677 CTAAGAAACAATAAGAGGCGCAGTTCGAATAGTAAACACCTCGGAATTTGATCTTGGCG 736  
QY 962 AGAAGTGTGCCACAGCTCACTGTGTGTAACACTTGTGATTTCTTGCAGATGAACGATGCCA 1021  
DB 737 AGAAGTGTGCCACAGCTCACTGTGTGTAACACTTGTGATTTCTTGCAGATGAACGATGCCA 796  
QY 1022 TAACTTTGCTACTGAGAAACAAATAAATCATGAGACATGGAATCAATAAATA 1081  
DB 797 TAACTTTGCTACTGAGAAACAAATAAATCATGAGACATGGAATCAATAAATA 856  
QY 1082 TGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGTCGTCTACCAATAGCAATCTTA 1141  
DB 857 TGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGTCGTCTACCAATAGCAATCTTA 916  
QY 1142 CAATAGGAGCTGTCTGCACTAAACAGGTCGAGAAATGGGAGAAATCTATGAACACC 1201  
DB 917 CAATAGGAGCTGTCTGCACTAAACAGGTCGAGAAATGGGAGAAATCTATGAACACC 976  
QY 1202 TTCCTTTGAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGAAATGGTCACTAG 1261  
DB 977 TTCCTTTGAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGAAATGGTCACTAG 1036  
QY 1262 GTTACAAACCACTACCTCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTCCCTG 1321  
DB 1037 GTTACAAACCACTACCTCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTCCCTG 1096  
QY 1322 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATCGATAGCAGAAAGGTTTGTTA 1381  
DB 1097 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATCGATAGCAGAAAGGTTTGTTA 1156  
QY 1382 GACCAAGGTTGGGATGAGCTAAGGATGTCGAGAGAACTTACTTTAATGAGCTAATCA 1441  
DB 1157 GACCAAGGTTGGGATGAGCTAAGGATGTCGAGAGAACTTACTTTAATGAGCTAATCA 1216  
QY 1442 ACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGCA 1501  
DB 1217 ACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGCA 1276  
QY 1502 TTCATGATATCATCGTGATATCAAGTTCGAATCTCGAGACAGGAAAAATTTGTATTAT 1561  
DB 1277 TTCATGATATCATCGTGATATCAAGTTCGAATCTCGAGACAGGAAAAATTTGTATTAT 1336  
QY 1562 TACCAATGGGAGATGGCTCTGATTTAGTTAGTTCAGGAAAACTTCGCCACATAGCAATCCATG 1621  
DB 1337 TACCAATGGGAGATGGCTCTGATTTAGTTAGTTCAGGAAAACTTCGCCACATAGCAATCCATG 1396  
QY 1622 GGAGTATGCTTCGCAAACTGGATTTGAGTTCGAGCATTTTCCGATCATTAGCTATTTTTGG 1681

Db 1397 GGAGTATGCTCTGCAAAACAGGATTTGGATTGGAGCAATTAATTCGATCAATAGCTAATTTTGG 1456  
 Qy 1682 GTGACAGACCCAGAGCTTAGCAGCATGCACTGAGTTTGGTCCAGATCAATTCAGAGATGTTACGGG 1741  
 Db 1457 GTGACAGACCCAGAGCTTAGCAGCATGCACTGAGTTTGGTCCAGATCAATTCAGAGATGTTACGGG 1516  
 Qy 1742 TCTTGGATCTTGAAGATGTCACATTTTAATCACTCAAAAAGATTTCCGACCGTATTGCAAT 1801  
 Db 1517 TCTTGGATCTTGAAGATGTCACATTTTAATCACTCAAAAAGATTTCCGACCGTATTGCAAT 1576  
 Qy 1802 TGTGTGCGCACTTTGAATTAATCTTGGATTTGGATTTGGTCAATCAATATATTTCACTTCCCA 1861  
 Db 1577 TGTGTGCGCACTTTGAATTAATCTTGGATTTGGATTTGGTCAATCAATATATTTCACTTCCCA 1636  
 Qy 1862 GATCCATTTGTAACTTACAGGCGCTTCAAACTTTGAAATGCGGAGACATATATTTGCGAG 1921  
 Db 1637 GATCCATTTGTAACTTACAGGCGCTTCAAACTTTGAAATGCGGAGACATATATTTGCGAG 1696  
 Qy 1922 CACTCCAGTGGAGATCAGTAACCTCAATGCTGCTACATCTTCTGTTGTATAGGACAGT 1981  
 Db 1697 CACTCCAGTGGAGATCAGTAACCTCAATGCTGCTACATCTTCTGTTGTATAGGAGT 1756  
 Qy 1982 TTCATTTATGACAACTTTAGTCTTAAACCCCAATGAAGTGCATTAACCAATATGCC 2041  
 Db 1757 TTGTTTCTGACAACTTTAGTCTTAAACCCCAATGAAGTGCATTAACCAATATGCC 1816  
 Qy 2042 TGCTTAAGTATTACACCTTTTGTAGTTCGGATGATCGTGAACCAATTTGCTGAAT 2101  
 Db 1817 TGCTTAAGTATTACACCTTTTGTAGTTCGGATGATCGTGAACCAATTTGCTGAAT 1876  
 Qy 2102 TGCACTAGGCGCAAAAGTTGCTGCTGAATCAATCGTGTGAAGGTACCCCAAGGAA 2161  
 Db 1877 TGCACTAGGCGCAAAAGTTGCTGCTGAATCAATCGTGTGAAGGTACCCCAAGGAA 1936  
 Qy 2162 TAGTAAAGTTGCGAGACTTGCAGGTTCTAGATGATAGATATCAGGCGACAGTAGTA 2221  
 Db 1937 TAGTAAAGTTGCGAGACTTGCAGGTTCTAGATGATAGATATCAGGCGACAGTAGTA 1996  
 Qy 2222 GAGCAATCAAAAGAGCTGGGCGCAGTTAAGCAAGCTGAGGAATTTAGTGTGACAAACG 2281  
 Db 1997 GAGCAATCAAAAGAGCTGGGCGCAGTTAAGCAAGCTGAGGAATTTAGTGTGACAAATG 2056  
 Qy 2282 GGTGCAAAAGGAAAATGTAGATATTTTGAAGCAATTTGAGAGCTCTTCTCCCTCC 2341  
 Db 2057 GGTGCAAAAGGAAAATGTAGATATTTTGAAGCAATTTGAGAGCTCTTCTCCCTCC 2116  
 Qy 2342 AATCTCTCCATGTTGATGCTGCGAGGAATCTCAGATGTTGGAACATTTGAGTGTCTAGATT 2401  
 Db 2117 AATATCTCTATGTAATGCTGCGAGGAATCTCAGATGTTGGAACATTTGAGTGTCTAGATT 2176  
 Qy 2402 CTATTTCAATCTCTCTCCCTACTGAGGACACTCGTGTGAGATGGAATTTCTTGAGGAGA 2461  
 Db 2177 CTATTTCTCTCTCTCCCTACTGAGGACACTCGTGTGAGATGGAATTTCTTGAGGAGA 2236  
 Qy 2462 TGCTTAATGTTGAGAGCTCACTCACTCAAGAGATCTACTTATTTGAGGAGCAAAAC 2521  
 Db 2237 TGCTTAATGTTGAGAGCTCACTCACTCAAGAGATCTACTTATTTGAGGAGCAAAAC 2296  
 Qy 2522 TAAAGGAAGTAAACCATGCTGATATTTGGGGGCTCGCCCAACTCATGTTCTTCTATC 2581  
 Db 2297 TAAAGGAAGTAAACCATGCTGATATTTGGGGGCTCGCCCAACTCATGTTCTTCTATC 2356  
 Qy 2582 TTTATCGGAATGTTACTTCTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAATC 2641  
 Db 2357 TTTATCGGAAGCTTACTTCTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAATC 2416  
 Qy 2642 TTAGAACATCTTTCGATTTATGAAATTTGATTCAGTCAAGAGATATGAGATTTGAGGAGCGCA 2701  
 Db 2417 TTAGAACATCTTTCGATTTTTCGATTTTTCGATTCAGTCAAGAGATTTGAGATTTGAGGAGCGCA 2476  
 Qy 2702 GCTCACCCTCTTGGGAAAATAGATAGAGTGGAGGAGTGGAGTTGGAATCTGGGATTAATCTG 2761  
 Db 2477 GCTCACCCTCTTGGGAAAATAGATAGAGTGGAGGAGTGGAGTTGGAATCTGGGATTAATCTG 2536

Qy 2762 GTATCATTCACCTTCCAAAGCTCAAGGAGATTCCAAATTAGATACGGAAGTAAAGTGGCTG 2821  
 Db 2537 GTATCATTCACCTTCCAAAGCTCAAGGAGATTCCAAATTAGATACGGAAGTAAAGTGGCTG 2596  
 Qy 2822 GGCTTGGTCACTGAGGAGGAGTGAACGACACCCAAATTCGCCCTGCTGCTAATGT 2881  
 Db 2597 GGCTTGGTCACTGAGGAGGAGTGAACGACACCCAAATTCGCCCTGCTGCTGGAAGA 2656  
 Qy 2882 ACAGTGACCAAGGATATCAAGCTGGGGGTGAAGCGGAGGATCTTCTATGAGAGTGC 2941  
 Db 2657 GGGAGGACCGAAGTATCAGACCTTGTCTGTGACGCGGAGGATCCCTGTTGAAGTGG 2716  
 Qy 2942 AAACAGACATCTGTTCTGATGCCGAGGA 2973  
 Db 2717 AAGCAAGGATCCCTCCAGAGGAGGGA 2748

RESULT 10

US-10-437-963-2483  
 ; Sequence 2483, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 2483  
 ; LENGTH: 2982  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102251C.1  
 ; US-10-437-963-2483

Query Match 60.7%; Score 1882; DB 7; Length 2982;  
 Best Local Similarity 78.9%; Pred. No. 0;  
 Matches 2352; Conservative 0; Mismatches 445; Indels 183; Gaps 2;

Qy 1 ATGCGCGAGACGCTGCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCATCAGCAAGGCC 60  
 Db 178 ATGCGCGAGACGCTGCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCATCAGCAAGGCC 237  
 Qy 61 GCCTCCGCTGCTGCCGAGAGACAGCTCTCTGCTGGCGCTGCGAGAGACATCTGGTAT 120  
 Db 238 ACCTCTGCGCGCGCCATGAGCGAGCTCTCTACTCTGCGCGTCCAGAGAGACATCTGGTAT 297  
 Qy 121 ATCAAGATGAGCTAAACAGATGCAACATTTCTTGAAGCTGCTGAACTTATGAAAAG 180  
 Db 298 ATCAAGATGAGCTAAACAGATGCAACATTTCTTGAAGCTGCTGAACTTATGAAAAG 357  
 Qy 181 AAGATGAACTATTAAAGTTTGGCAGAGCAAAATAGCTGACCTGTCTATGACATTTGAA 240  
 Db 358 AAGATGAGCTCTTAAAGTTTGGCAGAGCAAAATAGCTGACCTGTCTATGACATTTGAA 417  
 Qy 241 GATTCTCTGATGAAATTTTAAAGTTCATATTCAGGCGCAAAATCTTCTGCTGCTG 300  
 Db 418 GATTCTCTGATGAAATTTTAAAGTTCATATTCAGGCGCAAAATCTTCTGCTGCTG 477  
 Qy 301 AATCTCAGAGAGCGCCAGATTCCTATTCGATATTCACAACTTAAATCAAGAGTTGAA 360  
 Db 478 AAGCTCAGAGAGCGCCAGATTCCTATTCGATATTCACAACTTAAATCAAGAGTTGAA 537

QY 361 GAAGTGTAGCAGACACACGCTACAGTTTGTAGTCAAGCTATTCTCTGGCAGAG 420  
DB 538 GAAGTGTAGCAGAACTCAGCTACATTTAGTCAACCTATTTCATCCAGCAATGAG 597  
QY 421 ATTGACATGGATTCCTATGACAGAGACATTCGTAATCAGTCACTCGCAATGTGGATGAG 480  
DB 598 GATGACATGGATTTGTACGAGAGACATTCGTAATCAGTCACTAGCAATGTAGATGAA 657  
QY 481 GCTGAGCTTGTGGGTTTCTGACTCCAGAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
DB 658 ACTGAGCTTGTGGGTTTCTGACTCTAAGAT 690  
QY 541 GCTAATGATGTCGCGCAAGGTAATCTGTGTGTGTGGATGGTGTGGTTAGGCAAGACA 600  
DB 691 ----- 690  
QY 601 GCTCTTTCGAGGAGATCTTTGAAGCGAGAGACATTTAGGAAGAACTTCCCTTGGCAAT 660  
DB 691 ----- 690  
QY 661 GCTTGGATTACAGTGTCAATCATTTACAGGATTGACTACTTAAAGATATGATAGC 720  
DB 691 -----AGGATTGAGCTACTCAAGATATGATACGG 720  
QY 721 CAACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTCAGAGAAATTCAGAGGAGGTTGGT 780  
DB 721 CAAATTTCTAGGTTCCAAATCACTGGATCAAGTCTTCAGAGAAATTCAGAGGAGGTTGGT 780  
QY 781 GTGCAAGTACATCATCTTTCTGAGTACTCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 840  
DB 781 GTGCAAAATACCTCATCTTTCTGACTCTTGAGAGAAAGCTCAAGGAGAGAGGTATTTT 840  
QY 841 GTTGTCTTAGATGATCTATGGATTTTACATGATGGAATGTGAATGAATGAATGCAATTT 900  
DB 841 GTTGTCTTAGATGATCTATGGTCTTTAGATGCAATGGAATGAATGAATGCAATTT 900  
QY 901 CCTAAGACAATAAGAGGCGAGTCAAGTAAATAGTAATCAACCTCGGAATGTTGATCTTGGC 960  
DB 901 CCTAAGATNACAAATAGGCGAGTGGATTTAGTAACCAACAGAGATTTGGTCTAGCC 960  
QY 961 GAGAGTGTGCGACAGCTCTAGTGTGTACACCTTGATTTCTTCAGATGAACGATGCC 1020  
DB 961 GAGAGTGTACCAACCTTCCCTAGTCTACCATCTTTGAACATTCGAGATGAATGATGCC 1020  
QY 1021 ATAACTTTGCTACTGAGAGAAAACAAATAAAAATCATGAAGACATGGAATCAAAATAAAAT 1080  
DB 1021 ATAACTTTGCTACTGAGAGAAAACAAATAGAACATGAGACATGGAGAACAAACAAAT 1080  
QY 1081 ATGCAAAAGATGTTGAACGAATTTGAATTAATGTTGGTCTACCATTTAGCAATACTT 1140  
DB 1081 ATGCAAAAGATGTTGAACGAATTTGAATTAATGTTGGTCTACCATTTAGCAATACTT 1140  
QY 1141 ACAATAGAGCTGTGCTTGCATTAACAGTGTCAAGATGGGAGAGAAATTTCTATGAACAC 1200  
DB 1141 ACAATAGAGCTGTGCTTGCATTAACAGTGTCAAGATGGGAGAGAAATTTTATAAACAG 1200  
QY 1201 CTTCTTCAGAACTAGAAATTAACCCAGCTCGAAGCTTTGAGAGAGATGGTGACCTTA 1260  
DB 1201 CTTCTTCAGAACTAGAAATTAACCCAGCTTTCAAGCTTTGAGAGAGATGGTGACCTTT 1260  
QY 1261 GTTTACAACTACCATCCATTTGAAACCACTGCTTTTGTATCTAAGTATCTTTCCCT 1320  
DB 1261 GCTTACAACTACCATCCATTTGAAACCACTGCTTTTGTATCTAAGTATCTTTCCCT 1320  
QY 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTGGTAGATGATGAGAGAGGTTTGT 1380  
DB 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTGGTAGATGATGAGAGAGGTTTGT 1380  
QY 1381 AGACCAAAAGGTTGGATGACGACTAAGGATGTCCGAGAGAAAGTTACTTTAATGAGCTAATC 1440  
DB 1381 AGACCAAAAGGTTGGATGACGACCAAGGATGTGGGAGACAGTTACTTTAATGAGCTAATC 1440  
QY 1441 AACCGAAGTATGATTTCAACGATCAAGAGTGGGAGATAGCGAGGAGAAATTAAGACTTGTGCA 1500

DB 1441 AACCGAAGTATGATTTCAAGATCAAGAGTGGGCAATAGAGGAGGAAATTAAGAGTTGCCGA 1500  
QY 1501 ATTCAATGATATCATCGTGTATATCAAGTTTCAATCTCGAGACAGGAGAAATTTGTATTATTA 1560  
DB 1501 GTCCATGATATCATCGTGTATATCAAGTTTCAATCTTAGAGAGGAGAACTTTGTATTATTC 1560  
QY 1561 TTACCAATGGAGATGGCTCTGATTTAGTTTCAAGGAGAAACACTCGCCACATAGCATTTCCAT 1620  
DB 1561 TTACCAATGGAGATGGCTCTGATTTCAATCTTAGCAGAGGAGAAACACTCGCCACATAGCATTTCCAT 1620  
QY 1621 GGGAGTATGCTTGGGAAACTGGATTTGGAGCATTTTCCATCATTAGCTATTATTTT 1680  
DB 1621 GGGAGTATGCTTGGGAAACTGGAGTTGGAGCATTTTCCATCATTTAGCTATTATTTT 1680  
QY 1681 GGTGACAGACCCCAAGAGTCTTAGCAGATGCAATGTCAGATCAATTTGAGGATGTTACGG 1740  
DB 1681 GGTGACAGACCCCAATTAATCTTAGCAGACACATTTTCTCAATTAATTTCAAGATGTTACGG 1740  
QY 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTGACCGTATTGCA 1800  
DB 1741 GTCTTGGATCTTGAAGATGTGAGTTTAAATCAACAAAGATTTTCAATCATATATATAC 1800  
QY 1801 TTGTTGTGCCACTTTGAAATACTTTGAGTATTGG-----ATATTCGTCAATCCATATATTCA 1854  
DB 1801 TTGTTGTGCCACTTTGAAATACTTTGAGTATTGGAGGAAATTTCTCATCATATATATAC 1860  
QY 1855 CTTCCAGATTCATTTGGTAAACTTACAGGCTTACAACTTTGAACTCCGAGCACATAC 1914  
DB 1855 CTTCCAGATTCATTTGGTAAACTTACAGGCTTACAACTTTGAACTCCGAGCACATAC 1914  
QY 1915 ATTGACAGCTTACCAAGTGTGAGTCAAGTAACTTCCAAATGCTTGCATCTCTTCTTGTGATA 1974  
DB 1915 ATTGACAGCTTACCAAGTGTGAGTCAAGTAACTTCCAAATGCTTGCATCTCTTCTTGTGATA 1974  
QY 1975 GGACAGTTTCATTTATGACAACTTTAGTCTAAACCAACCCAAATGAAGTGTCAATTAACACA 2034  
DB 1975 GGACAGTTTCATTTATGACAACTTTAGTCTAAACCAACCCAAATGAAGTGTCAATTAACACA 2034  
QY 2035 ATATGCTGCTTAAAGTATTTCACCTTTAGTTAGTTCGCGATGATCGTCAAAACAAAT 2094  
DB 2035 ATATGCTGCTTAAAGTATTTCACCTTTAGTTAGTTCGCGATGATCGTCAAAACAAAT 2094  
QY 2041 ATGTTCTGCTTAATTAATTTACACTTCNGTTAGTAGGACAACTTCGTCGCAACAAAT 2100  
DB 2041 ATGTTCTGCTTAATTAATTTACACTTCNGTTAGTAGGACAACTTCGTCGCAACAAAT 2100  
QY 2095 GCTGAATTTGACATGCGCCACCAAAAGTTCGCTGCTGAATCAATCGTGTGAGAGTACCC 2154  
DB 2095 GCTGAATTTGACATGCGCCACCAAAAGTTCGCTGCTGAATCAATCGTGTGAGAGTACCC 2154  
QY 2155 AAAGCAATAGTAAAGTTGGAGACTTTGCAAGTTCCTAGAGTATGTAGATATCAGGCGGACC 2214  
DB 2155 AAAGCAATAGTAAAGTTGGAGACTTTGCAAGTTCCTAGAGTATGTAGATATCAGGCGGACC 2214  
QY 2215 AGTAGTAGCAATCAAAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAGAAATAGGTGTGACA 2274  
DB 2215 AGTAGTAGCAATCAAAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAGAAATAGGTGTGACA 2274  
QY 2221 AGTACTAGTCAATCCAAAGAAATTTGGCGCACTTAAGCAAGCTGACTTAAATTAAGTGTGACA 2280  
DB 2221 AGTACTAGTCAATCCAAAGAAATTTGGCGCACTTAAGCAAGCTGACTTAAATTAAGTGTGACA 2280  
QY 2275 ACRAAGGCTGCAAAAGGAGAAATTTAGATTAATTTATGACGCAATTTGAGAAGCTCTCT 2334  
DB 2275 ACRAAGGCTGCAAAAGGAGAAATTTAGATTAATTTATGACGCAATTTGAGAAGCTCTCT 2334  
QY 2281 ACAAGGAGTCCACAGAGGAGAAATTTAGATTAATTTATGAGGCAATCCAAAGGCTCTGT 2340  
DB 2281 ACAAGGAGTCCACAGAGGAGAAATTTAGATTAATTTATGAGGCAATCCAAAGGCTCTGT 2340  
QY 2335 TCCCTCCAAATCTCTCCATGTGAGATGCTGAGGAATCTCAGATGCTGAGGAGAACTTTGAGTGC 2394  
DB 2335 TCCCTCCAAATCTCTCCATGTGAGATGCTGAGGAATCTCAGATGCTGAGGAGAACTTTGAGTGC 2394  
QY 2341 TCCCTGCAATCTCTCCGTTGGATGCTGAGGAGGCTCTCAGGAGAAATGGAACACTTAAATGT 2400  
DB 2341 TCCCTGCAATCTCTCCGTTGGATGCTGAGGAGGCTCTCAGGAGAAATGGAACACTTAAATGT 2400  
QY 2395 CTAGATTTCTATTTCT 2454  
DB 2395 CTAGATTTCTATTTCT 2454  
QY 2455 GAGGAGATGCTTAATCGATGAGAGCTCACTCACTGAGAGAGATCTTCTATTATGAGG 2514  
DB 2455 GAGGAGATGCTTAATCGATGAGAGCTCACTCACTGAGAGAGATCTTCTATTATGAGG 2514  
QY 2461 GAAAGATGCGCAACTGGATGAGAGCTCTCGCACCTCTCACTGAGGTTCTTCTATTATGAGG 2520  
DB 2461 GAAAGATGCGCAACTGGATGAGAGCTCTCGCACCTCTCACTGAGGTTCTTCTATTATGAGG 2520  
QY 2515 AGCAAACTAAGGAGGTAAGAAACCACTGCTGATTAATTTGGGCACTTCCCACTCATGTC 2574  
DB 2515 AGCAAACTAAGGAGGTAAGAAACCACTGCTGATTAATTTGGGCACTTCCCACTCATGTC 2574



Db 2521 AGTAACTAAAGAGGAAACCAATGCTGATCTTGGGCAATGCGCACTCATGCTG 2580  
 Qy 2575 CTTTCATCTTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTTCAAAAACAGAGCAATTC 2634  
 Db 2581 CTTTGTCTTTCACTTGATGCTTACCTCGGGGAGAAATCTAGTATTCAGAAACAGAGCAATTC 2640  
 Qy 2635 CCAATCTTTAGAACACTTTGGATTTATGAATGAGATCAGCTAGAGAGATCAGATTTGAG 2694  
 Db 2641 CAAAAGCTCAGGACACTTTGGTTTGCACAGCTGAGTACGCTAGAGAGATTTAGTTTGA 2700  
 Qy 2695 GACGAGAGCTCACCCCTGTTGAAAAGATAGAAATAGGAGTGCAGTTGGAAATCTGG 2754  
 Db 2701 AACGACAGCTCGCCCTATTGGAAGATAGAAATCGACTACGAGTTGGAAATAGGG 2760  
 Qy 2755 ATTACTGATATCAATTCACCTTCAAAAGCTCAAGGATTCMAATTAGATCAGGAATAA 2814  
 Db 2761 ATTATTGGTATCTTAACCTTATGAGGCTAAAGGAATTAACATTTGGATACAGATTA 2820  
 Qy 2815 GTGGCTGGGCTTGGTCACTGAGGAGAGAGTGAACGACACACCCCAATCGCCCGTGTG 2874  
 Db 2821 GTTGGTTATCTTGGTCAGTTGGAAGAGAGTTGGACACACCCCAATCGCCCGTGTG 2880  
 Qy 2875 CTAATGTACAGTACCGAAGGTATCAGACCTGGGGCTGAAGCGGAGGATCTTCTATA 2934  
 Db 2881 CGTATGAGGAGGACCGAAGCTGTACGACCTGAGAGGGATGCAAAAGGATCAGCTGTA 2940  
 Qy 2935 GAAGTGCAACACGACATCTGTCTGATGCGCGAAGGAT 2974  
 Db 2941 GAATGAGACCAAGGAGCCCTCTGAGCCGAGAGCT 2980

RESULT 11

US-10-656-394A-15  
 ; Sequence 15, Application US/10656394A  
 ; Publication No. US20040210957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang et al.  
 ; TITLE OF INVENTION: Cloning and Characterization of the  
 ; FILE REFERENCE: broad-spectrum resistance gene P12  
 ; FILE REFERENCE: 035718/252062  
 ; CURRENT APPLICATION NUMBER: US/10/656,394A  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 2422  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2226,  
 ; LOCATION: 2268, 2299, 2333, 2337, 2359, 2356  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-656-394A-15

Query Match 52.3%; Score 1621; DB 8; Length 2422;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1479 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCGTGATATCATGATTCATCAATTC 1538  
 Db 1 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCGTGATATCATGATTCATCAATTC 60  
 Qy 1539 GAGACAGGAAAAATTTTGTATTTATTAATGAGATGAGTCTGATTTAGTTAGTTAGGAAAA 1598  
 Db 61 GAGACAGGAAAAATTTTGTATTTATTAATGAGATGAGTCTGATTTAGTTAGTTAGGAAAA 120  
 Qy 1599 CACTCGCCACATAGCAATTCACCGGAGTATGTCCTGCAAACTGATTTGGATTGGAGCAT 1658  
 Db 121 CACTCGCCACATAGCAATTCACCGGAGTATGTCCTGCAAACTGATTTGGATTGGAGCAT 180  
 Qy 1659 TATTGATCATAGTATTTTGTGACAGACCCAGAGCTCTAGCACATGACGATTTCTCC 1718

Db 181 TATTCGATCAATTTAGCTATTTTGGTGACAGACCCAGAGCTTAGCACATGCACTTGTGTC 240  
 Qy 1719 AGATCAATTTAGGAGTGTACCGGCTTTGGATCTTGAAGATGTGACATCTTCTTAATCACTCA 1778  
 Db 241 AGATCAATTTAGGAGTGTACCGGCTTTGGATCTTGAAGATGTGACATCTTCTTAATCACTCA 300  
 Qy 1779 AAAAGATTTCCGACCCGATTTGCAATTTGTTGTGCACTTGAATTAATCTTGAATTTGATTTTC 1838  
 Db 301 AAAAGATTTCCGACCCGATTTGCAATTTGTTGTGCACTTGAATTAATCTTGAATTTGATTTTC 360  
 Qy 1839 GTCAATCATATTTCACTTCCAGATTCATTTGTTGTAATTAATCTTGAATTTGATTTTC 1898  
 Db 361 GTCAATCATATTTCACTTCCAGATTCATTTGTTGTAATTAATCTTGAATTTGATTTTC 420  
 Qy 1899 CATGCCGAGCACAATTTGAGCAGCTTACCAAGTGAATCAGTAAATCTTGAATTTGATTTTC 1958  
 Db 421 CATGCCGAGCACAATTTGAGCAGCTTACCAAGTGAATCAGTAAATCTTGAATTTGATTTTC 480  
 Qy 1959 TACTTCTGTTTATGAGCAGATTTTCAATTTATGACAACTTTTATGTTAAACCCCAATGAA 2018  
 Db 481 TACTTCTGTTTATGAGCAGATTTTCAATTTATGACAACTTTTATGTTAAACCCCAATGAA 540  
 Qy 2019 GTGCATAAATAACCAATATGCTGCTTAAAGTATTTCACTTTTATGTTAGTTCGCGATGA 2078  
 Db 541 GTGCATAAATAACCAATATGCTGCTTAAAGTATTTCACTTTTATGTTAGTTCGCGATGA 600  
 Qy 2079 TCGTGCAAAAATAATTTGCAATTTGCAATGCGCCCAACCAAGTTGCTGCTGATCAAT 2138  
 Db 601 TCGTGCAAAAATAATTTGCAATTTGCAATGCGCCCAACCAAGTTGCTGCTGATCAAT 660  
 Qy 2139 CGGTGTGAAGTACCCCAAGGAATAGTAAAGTTCGAGACTTTGAGGATTTCTAGAGTATGT 2198  
 Db 661 CGGTGTGAAGTACCCCAAGGAATAGTAAAGTTCGAGACTTTGAGGATTTCTAGAGTATGT 720  
 Qy 2199 AGATATCAGCGGACCACTAGTATGAGCAATCAAGAGCTGGGAGCTGAGTAAAGCTGAG 2258  
 Db 721 AGATATCAGCGGACCACTAGTATGAGCAATCAAGAGCTGGGAGCTGAGTAAAGCTGAG 780  
 Qy 2259 GAAATTTAGTGTGACAAACAGGCTGCAAAAGGAAATGTAAGATCTTTTATGCAAGC 2318  
 Db 781 GAAATTTAGTGTGACAAACAGGCTGCAAAAGGAAATGTAAGATCTTTTATGCAAGC 840  
 Qy 2319 CATTGAGAAAGCTCTCTTCCCTCAATCTCTCCATGTTGATGCTGCAAGAACTCTAGATGG 2378  
 Db 841 CATTGAGAAAGCTCTCTTCCCTCAATCTCTCCATGTTGATGCTGCAAGAACTCTAGATGG 900  
 Qy 2379 TGGAACTCTGAGTGTGATGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438  
 Db 901 TGGAACTCTGAGTGTGATGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960  
 Qy 2439 GTTGGATGGAATTTCTTGGAGGATGCTTAACTGGAATTTGAGCAGCTCTCACTCACTGAGAA 2498  
 Db 961 GTTGGATGGAATTTCTTGGAGGATGCTTAACTGGAATTTGAGCAGCTCTCACTCACTGAGAA 1020  
 Qy 2499 GATCTACTTATTTGAGGAGCAAACTAAAGAGGTAACCACTGATCTGATCTTGGGGCACT 2558  
 Db 1021 GATCTACTTATTTGAGGAGCAAACTAAAGAGGTAACCACTGATCTGATCTTGGGGCACT 1080  
 Qy 2559 GCCCAACCTCATGCTCTTCTTATCGGAATGCTTACCTTGGGGAGGAGCTAGTATTT 2618  
 Db 1081 GCCCAACCTCATGCTCTTCTTATCGGAATGCTTACCTTGGGGAGGAGCTAGTATTT 1140  
 Qy 2619 CAAAAAGAGGAGCAATTTCCAAATCTTGAACACTTTGGATTTATGAATTTGATCTAGCTTAAG 2678  
 Db 1141 CAAAAAGAGGAGCAATTTCCAAATCTTGAACACTTTGGATTTATGAATTTGATCTAGCTTAAG 1200  
 Qy 2679 AGAGATCAGATTTGAGGAGCGAGCTCACTCCCTGTTGGAAGATAGAAATAGGCGGAGTG 2738  
 Db 1201 AGAGATCAGATTTGAGGAGCGAGCTCACTCCCTGTTGGAAGATAGAAATAGGCGGAGTG 1260  
 Qy 2739 CAGTTGGAAATCTGGGATTTAGTGTATCACTTCCAAAGCTCAAGGAGATTTCAAT 2798  
 Db 1261 CAGTTGGAAATCTGGGATTTAGTGTATCACTTCCAAAGCTCAAGGAGATTTCAAT 1320







181 AAAGTGAACATTAATAAGGTTTGGGAGAGGAAATACGTGACCTGTCTATATGACATTGAA 240  
181 AAAGTGAACATTAATAAGGTTTGGGAGAGGAAATACGTGACCTGTCTATATGACATTGAA 240  
241 GATTCCCTTGAATGAAATTAAGGTTTGAATGAAAGGCAAAACCCCTATTTCGTCTAGTTGGTG 300  
241 GATTCCCTTGAATGAAATTAAGGTTTGAATGAAAGGCAAAACCCCTATTTCGTCTAGTTGGTG 300  
301 AAAGTGAACATTAATAAGGTTTGGGAGAGGAAATACGTGACCTGTCTATATGACATTGAA 360  
301 AAAGTGAACATTAATAAGGTTTGGGAGAGGAAATACGTGACCTGTCTATATGACATTGAA 360  
361 GAGTGTAGTAGAGGAAACACAGCTACAGTTTGTAGTCAAGCTTATTCCTCTGG --- CACA 417  
361 GAGTGTAGTAGAGGAAACACAGCTACAGTTTGTAGTCAAGCTTATTCCTCTGG --- CACA 420  
418 GAGTGTAGTAGAGGAAACACAGCTACAGTTTGTAGTCAAGCTTATTCCTCTGG --- CACA 477  
421 GAGGATGAGAGGAAATTCCTACCTAGAGATGCTGCAATCGATCAGGTAGCAACCTGAC 480  
478 GAGGCTGAGCTTGTGGGTTTCTGACTCCAGAGAAAGGCTGCTTGAAGATGATCGATACC 537  
481 GAGTGTAGTAGAGGAAACACAGCTACAGTTTGTAGTCAAGCTTATTCCTCTGG --- CACA 540  
538 AATGCTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGTGGATGGGTGGTGTAGGCAAG 597  
541 AATACTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGTGGATGGGTGGTGTAGGCAAG 600  
598 ACAGCTCTTTTCGAGGAGGAACTTTGAAAGCGAGAGGACATTTAGAGAGAACTTCCCTTGC 657  
601 ACTACCTTCCAGAGGAGGCAATGATGAAACAGGAAACAT --- GAGAACTTCTGTGT 657  
658 AATGCTGTAGTACAGTGTCAACATTTCAAGATGAGGTGAGTCTTTAAGATATGATA 717  
658 TGTGCTTGGATCACTGTGTCTCAGTCAITTTGACAGGAAAGAAATTTGCAAAACAAATGATC 717  
718 CGCAACTTCTGCGCCAGTCTCTGATCACTTGTGAGGAAATTTGCAAAACAAATGATC 777  
718 AGGCACTTCTGCGCCAGTCTCTGATCACTTGTGAGGAAATTTGCAAAACAAATGATC 777  
778 GTGCTGACATGATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTAC 837  
778 CTGCTGACATGATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTAC 837  
838 TTTGCTTGTAGATGATCTAGGATTTTACATGATTTGGAATTTGGAATTTGGAATTTGGA 897  
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898 TTTCTTGAAGAACATTAAGAGGCGAGTGGATTAATTAACCACTCGGAATTTGATCTT 957  
898 TTTCTTGAAGAACATTAAGAGGCGAGTGGATTAATTAACCACTCGGAATTTGATCTT 957  
958 GCGGAGAGGTTGCGACAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1017  
958 GCTGGAAGGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017  
1018 GCTATACATTTGCTAGTCAAGAGCAAAATTAAGATTTGGAATTTGGAATTTGGAATTTGGA 1077  
1078 AATATGCAAAAGATGTTGAAAGATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAAT 1137  
1078 GACTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137  
1138 CTTCATATAGGAGGATTTCTGCTACTAAGAGATTAATGGAATTTGGAATTTGGAATTTGGA 1197  
1138 CTTCATATAGGAGGATTTCTGCTACTAAGAGATTAATGGAATTTGGAATTTGGAATTTGGA 1197  
1198 CACTTCTTCTAGAACTAGAAATTAACCAAGCTTGGAGGAGGATTTGGAATTTGGAATTTGGA 1257  
1198 GAACTTCTTCTAGAACTAGAAATTAACCAAGCTTGGAGGAGGATTTGGAATTTGGAATTTGGA 1257

1258 CTAGGTTTCAACCACTACCATCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTT 1317  
1258 CTAGGTTTCAACCACTACCATCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTT 1317  
1318 CTGAGGATTTTGAATCAAAAGGAAATCTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1377  
1318 CTGAGGATTTTGAATCAAAAGGAAATCTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1377  
1378 GTTATGACCAAAAGGTTGGGATGACGACTAAGGATGCTCGGAGAAAGTTTAAATGAGCTA 1437  
1378 GTTATGACCAAAAGGTTGGGATGACGACTAAGGATGCTCGGAGAAAGTTTAAATGAGCTA 1437  
1438 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGATGAGGAGAAATTTAAGACTTGT 1497  
1438 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGATGAGGAGAAATTTAAGACTTGT 1497  
1498 CGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGAGGAAATTTTGT 1557  
1498 CGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGAGGAAATTTTGT 1557  
1558 TTATTAACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCACATAGCATTC 1617  
1558 CTGTTCACTAGGAGAAAGATCACTGTTGTAGCGGAGGAGGAGCATCCGCCATCTAGCATTT 1617  
1618 CATGGAGTATCTCTGCGCAAACTGATTTGATTTGAGGATTTTCAATCTCGAGAGGAAATTT 1677  
1618 CATGGAGTATCTCTGCGCAAACTGATTTGATTTGAGGATTTTCAATCTCGAGAGGAAATTT 1677  
1678 TTTGTTGAGCAGACACCCCAAGAGTGTAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737  
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1738 CGGCTTCTGATTTGAGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 1797  
1738 AGAGTGTGATTTGAGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 1797  
1798 GCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857  
1798 GGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857  
1858 CCAGATTCATTTGTTGATGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTT 1917  
1858 CCAGATTCATTTGTTGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 1917  
1918 GCAGACTTACCAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1977  
1918 TCAGACTTACCAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1977  
1978 CAGTTTCATTTGATGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 2034  
1978 CAGTTTCATTTGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 2034  
1978 AGGTGAGTGTGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 2037  
2035 ATATGCTGCTTAAAGTATTTCACTTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2094  
2038 ATGCTGCTTAAAGTATTTCACTTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2097  
2095 GCTGAAATTTGATGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 2154  
2098 CTTGAGATGATGATGATTTTCACTTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2157  
2155 AAAGGAAATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2214  
2158 AGAGGAAATTTGATGATGATTTTCAATCTCGAGAGGAAATTTTCAAGGATTTTCA 2217  
2215 AGTGTGTAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2274  
2218 AGTGTGTAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2277  
2275 ACAAACGGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2334  
2278 ACAAACGGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 2337  
2335 TCCCTCCAATCTCTCATGTTGATGCTGCTGAGGAAATCTCAGATGTTGGAACACTTTGAGTGTGC 2394



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1140 TACAATAGGAGCTGTGCTTGCACATTAACAGAGTGTGACAGATGGGAGAAATTTATGACAA 1199
1143 CACAATAGGAGGCAATCTTCTACTAAGAGATAATAGGAGTGGGAGAAATTTTACAGAGA 1202
1200 CTTTCTTTAGAACTAGAAATAAACCAAGCTGGAAGCTTTTGGAGAGATGGTGACCTT 1259
1203 ACTTCTTTAGAGCTTGAAGCAGATCCAGCTTAGAGCCATGAGGAGATGGTGACCTT 1262
1260 AGGTTACAAACCTACCTACCTATTTGAAACATGCTTTTGTGTATCTAAGTATCTTTCC 1319
1263 AAGCTACAATCACTTACCATCTCATCTTAAACCATGCTTTCTTTACCTAAGTATTTTCCC 1322
1320 TGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATGGATAGCAGAGGTTTGT 1379
1323 TGAAGATTTTGAATTTCAAGAGGGGCGCTTGTAGATAGATAGATAGCAGAGGTTTGT 1382
1380 TAGACCAAGGTTGGGATAGCAGTAAAGATGTGCGAGAAAGTTTACTTTTATGAGCTTAT 1439
1383 CAGAGCCACAGATGGGTTGAACATTCAGGATGTGGAAATAGTCACATTTTATGAGCTTAT 1442
1440 CAACCGAAGTATGATTCACAGATCAAGAGTGGGCTAGCAGGAAATTTAAGACTTGTG 1499
1443 CAACAGAGTCTGATTCAGGCTTCAAAAGTTAGTACAGATGGAGTTGTAAAGATGTG 1502
1500 AATTCATGATATCATCGTGATATCAAGTTCATCTCGAGACAGAGAAATTTTGTATTT 1559
1503 AATCCATGATATCATCGTGATATCATGTTTCAATTTCTAGAGAGGAAATTTTGTGCT 1562
1560 ATTACCAATGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCACATAGCATTTCCA 1619
1563 GTTCACTAGGAGAGATCACTGTTGTAGCGAGAGAGATCCGCCATCTAGCATTTTCA 1622
1620 TGGAGATATGCTTCAAACTCGATTTGATTTGAGTGTGAGCATTTTATGATCATTTT 1679
1623 TGGAGCAAAATGCTTCAAGATATGCTTGGAGTGAACCATCTGGGCTCAGTAACTTTGTT 1682
1680 TGGTACAGAGCCCAAGAGTCTAGCAGATGAGTTTGTCCAGATCAATTTGAGGATGTTAAG 1739
1683 TGGCAGACAGCTGTGGGGGAGACACTGCACTTTGTTTCAACAAATTTAGGATGCTGAG 1742
1740 GGTCTTGATCTTGAAGATGACATCTTTTAACTCACTCAAAAGATTTGACCGTATTTG 1799
1743 AGTGTGATCTGGAAGATGCAAAATTCAAATTCACAAATGATATCAGGAATATAGG 1802
1800 ATTGTGTGACCTTGAATATCTTGAATTTGATATGATATGCTCATCCATATATTCACATTTCC 1859
1803 GTTGTGCGCCACATGAATATTTGAATTTTGAAGGCTCACTATTTATACACTTCC 1862
1860 CAGATCCATTTGTTAACTACAGGGCTTCAAACTTTGAACTGCGAGCACATACATTTGC 1919
1863 AAGTCCATAGGAAATTTGAGTGTGCAATTTTGAACATGAGGAGGCAAAATATCTC 1922
1920 AGCACTACCAAGTACAGATAGTAACTCCAAATGCTGATATCTTCTGTTGATAGGACA 1979
1923 AGCACTACCAAGTACAGATAGTAACTCCAAATGCTGATATCTTCTGTTGATAGGACA 1982
1980 GTTTCATTTAGCAACTTTTATGCTTAA---ACCAACCAATGAGTGCATATCACTAACAAT 2036
1983 GTCTGTTTCTGTTTACTTTAGCATAATAGATAATCCCAAGGAATCTTTGATGATCACCAT 2042
2037 ATGCTGCTTAACTATTCACCTTTTGTAGTGTGATGATGATGATGATGATGATGATGATG 2096
2043 GTGCTTACCGATGTTTCTTAACTTCAATTAATTTTCAATGATGATGATGATGATGATGATG 2102
2097 TGAATTCAGATGCGCCACCAAAAGTTGCTGTTGATCAATCAATCGGTGTGAAGGTACCCAA 2156
2103 TGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2162
2157 AGGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2216
2163 AGGAATTCAGAACTTAAAGAGTTACAGATTTCTAGAAAGTCTGTTGAGATCAACAGAACTAG 2222
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## RESULT 15

US-10-656-394A-1  
; Sequence 1, Application US/10656394A  
; Publication No. US20040210957A1

## GENERAL INFORMATION:

; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; TITLE OF INVENTION: broad-spectrum resistance gene Pi2  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ... (2982)  
US-10-656-394A-1

Query Match 50.1%; Score 1553.4; DB 8; Length 2982;  
Best Local Similarity 71.5%; Pred. No. 0;





GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 21:31:07 ; Search time 895 Seconds  
(without alignments)  
7989.177 Million cell updates/sec

Title: US-10-656-394A-7  
Perfect score: 3099  
Sequence: 1 atggcgagacggtgctgag.....scacagctcaagctggtgta 3099

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
1: /cgn2\_6/prodata/1/pubna/US08 NEW\_PUB.seq:  
2: /cgn2\_6/prodata/1/pubna/US06 NEW\_PUB.seq:  
3: /cgn2\_6/prodata/1/pubna/US07 NEW\_PUB.seq:  
4: /cgn2\_6/prodata/1/pubna/PCT NEW\_PUB.seq:  
5: /cgn2\_6/prodata/1/pubna/US05 NEW\_PUB.seq:  
6: /cgn2\_6/prodata/1/pubna/US03 NEW\_PUB.seq:  
7: /cgn2\_6/prodata/1/pubna/US10 NEW\_PUB.seq:  
8: /cgn2\_6/prodata/1/pubna/US10 NEW\_PUB.seq:  
9: /cgn2\_6/prodata/1/pubna/US11 NEW\_PUB.seq:  
10: /cgn2\_6/prodata/1/pubna/US11 NEW\_PUB.seq:  
11: /cgn2\_6/prodata/1/pubna/US11 NEW\_PUB.seq:  
12: /cgn2\_6/prodata/1/pubna/US11 NEW\_PUB.seq:  
13: /cgn2\_6/prodata/1/pubna/US60 NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107.8	3.5	2151	9 US-11-031-206-125	Sequence 125, App
2	80.6	2.6	644	9 US-11-031-206-107	Sequence 107, App
3	79.8	2.6	1944	9 US-11-031-206-109	Sequence 109, App
4	79	2.5	1902	9 US-11-031-206-137	Sequence 137, App
5	75.2	2.4	1861	9 US-11-031-206-115	Sequence 115, App
6	67.8	2.2	306	9 US-11-031-206-123	Sequence 123, App
7	49.6	1.6	813	9 US-11-031-206-127	Sequence 127, App
8	48	1.5	634	9 US-11-031-206-139	Sequence 139, App
9	43	1.4	590	9 US-11-031-206-135	Sequence 135, App
10	41	1.3	879	6 US-09-925-065A-284566	Sequence 284566
11	40.8	1.3	507	9 US-11-031-206-117	Sequence 117, App
12	40.6	1.3	469	6 US-09-925-065A-284567	Sequence 284567
13	40.6	1.3	469	6 US-09-925-065A-284568	Sequence 284568
14	40.2	1.3	625	6 US-09-925-065A-107964	Sequence 107964
15	40.2	1.3	625	6 US-09-925-065A-107965	Sequence 107965
16	39.8	1.3	625	6 US-09-925-065A-107966	Sequence 107966
17	39.6	1.3	1103	6 US-09-925-065A-81285	Sequence 81285, A
18	39.4	1.3	563	6 US-09-925-065A-287089	Sequence 287089, A
19	39.4	1.3	20945	8 US-10-995-561-13463	Sequence 13463, A
20	39.4	1.3	23082	8 US-10-995-561-13457	Sequence 13457, A

21	39	1.3	563	6 US-09-925-065A-287087	Sequence 287087,
22	39	1.3	563	6 US-09-925-065A-287088	Sequence 287088,
23	38.8	1.3	540	6 US-09-925-065A-794000	Sequence 794000,
24	38.8	1.3	601	6 US-09-925-065A-814272	Sequence 814272,
25	38.8	1.3	605	6 US-09-925-065A-810341	Sequence 810341,
26	38.4	1.2	601	6 US-09-925-065A-736743	Sequence 736743,
27	38.4	1.2	605	6 US-09-925-065A-730236	Sequence 730236,
28	38.4	1.2	2310	6 US-09-925-065A-686675	Sequence 686675,
29	38.2	1.2	208765	7 US-10-330-773-407	Sequence 407, App
30	38	1.2	619	6 US-09-925-065A-511863	Sequence 511863,
31	38	1.2	622	6 US-09-925-065A-105078	Sequence 105078,
32	37.6	1.2	540	6 US-09-925-065A-850087	Sequence 850087,
33	37.6	1.2	627	6 US-09-925-065A-761303	Sequence 761303,
34	37.6	1.2	633	6 US-09-925-065A-811922	Sequence 811922,
35	37.6	1.2	1041	6 US-09-925-065A-723466	Sequence 723466,
36	37.6	1.2	1041	6 US-09-925-065A-723467	Sequence 723467,
37	37.4	1.2	524	6 US-09-925-065A-148152	Sequence 148152,
38	37.4	1.2	524	6 US-09-925-065A-148153	Sequence 148153,
39	37.2	1.2	562	6 US-09-925-065A-424975	Sequence 424975,
40	37.2	1.2	607	6 US-09-925-065A-381464	Sequence 381464,
41	37	1.2	2723	6 US-09-925-065A-69776	Sequence 69776, A
42	37	1.2	2723	6 US-09-925-065A-69777	Sequence 69777, A
43	37	1.2	4777	12 US-11-136-327-218	Sequence 218, App
44	36.8	1.2	547	6 US-09-925-065A-314610	Sequence 314610,
45	36.8	1.2	573	6 US-09-925-065A-380787	Sequence 380787,

ALIGNMENTS

RESULT 1

US-11-031-206-125  
; Sequence 125, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Rua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; FILE REFERENCE: BB1357 US NA  
; CURRENT APPLICATION NUMBER: US/11/031,206  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 125  
; LENGTH: 2151  
; TYPE: DNA  
; ORGANISM: Glycine max

US-11-031-206-125

Query Match	3.5%	Score 107.8	DB 9	Length 2151
Best Local Similarity	48.1%	Pred. No. 5.7e-18		
Matches 415	Conservative 0	Mismatches 427	Indels 21	Gaps 3
QY	558	CAAGGTAACTGTGTTGTTGGGATGGTGGTTTAGCGAAGACAGCTCTTTTCGAGGAAGAT	617	
DB	1301	CACCATCATCTTTGTGTAGGATGGAGGGCTAGGAAACCACTGTTGCCGAAGAGT	1360	
QY	618	CTTTGAAAGCGAAGACACATTAAGGAAGACTTCCTCTTGCAATGCTTTGGATATACAGTTC	677	
DB	1361	CTTCAATAACCGAAGGTGATT---GCACACTTTGATTGCCATGATGATGATCACAAGTTC	1417	
QY	678	ACAATCATTTTCACAGGATTCAGCTACTTAAAGATATGATCGCCAACTCTTTGGSCCCAG	737	
DB	1418	TCATATCTTCACTGTGGAAGGGTGTCTAGAGACTTGTGAAGACTTATTGCAAGATTATGCAAGAAA	1477	
QY	738	TTCTCTGGATCAACTCTTTGCAAGAAATTGCAAGGAGGTGGTGGTGGCAAGTACATCATCT	797	
DB	1478	GAAAGTGGATCCTCCT-----CATGATATTTCTGAAATGATTCGAGATTCACCT	1525	
QY	798	TTCTGAGTACCTGATACGAGCTCAAGGAGAGAGGTACTTTTGTGTTCTAGATGATCT	857	
DB	1526	GATTGATGAAGTGAGAGCCATTTCGACGAAGAGAGTATGTTGTCTATTCTTTGATGATGT	1585	
QY	858	ATGGATTTTACATGATTGGAATTTGGATAAATGAAATTCGATTTCTCTAAGAACATTAAGAA	917	
DB	1586	ATGGAGTGTAGAACTTTGGGGTCAAATTCGAAATTCGATTCGTGATCTATGAAATGGTTG	1645	
QY	918	GGCGAGTCGATGATATACCACTCGGAATGTTGATCTTGGGAGAGGTGTCACAGC	977	
DB	1646	TAGAAATTAATCAACTAGGATGGATGGTGTGTGAGACTCTGTGATGAAATATCTCTTC	1705	
QY	978	CTCACTGGTGTACCACTTCGATTTCTTGCGAGATGAACGATGCCATAACATTCGTACTGAG	1037	
DB	1706	GGATAAGGTGCATAAGCTGAAACCTTTGACTCAAGAAGAACTCATGCAACTCTTTTGCA	1765	
QY	1038	AAAAACAAATAAAAATCATGAAGACATGGATCAATTAATAATATGCAAGAGATGGTTGA	1097	
DB	1766	GAAAGCATACCGATACCACAATTAATGGGCATTTGTCCAGAAGATCTTAAGAAAAATTTCTTC	1825	
QY	1098	ACGAATTTGAATAAATGTGGTGGTCTTACCATTAGCAATPACTTACAATPAGGAGCTGTGCT	1157	
DB	1826	TGACTTTGTTGAAAAATGTAAGGGTTTACCATTTGCCAATTTGGCTATTGTGATCTCTTT	1885	
QY	1158	TGCACTATAACAGGTG-----TCAGATGGGAGAAATTCATAGAACACTTCCTTCAGA	1211	
DB	1886	ATCTGGCAAGAAAGAACTCCATTTGAATGGGAAAAAATTAGCGAAGCCTTAAGTTCAGA	1945	
QY	1212	ACTAGAAATAAACCCAGCCTGGNAGCTTTGAGGAGAAATGGTGACCTTAGCTTACCAACCA	1271	
DB	1946	GATGAACAAAGTCCCAATTAATTTGGCATACCAAGATTTTAGTTCAGTTATGATGA	2005	
QY	1272	CCTACCATCCCATTTGAAAAACATGCTTTTGTATCTTAAGTATCTTTCTCGAGGATTTTGA	1331	
DB	2006	TTTGCCATATTATCTGAAATCATGCTTATTGTATTTTGGTGTATATCCGGAAGCATATGA	2065	
QY	1332	AATCAAAAGGAATCGTCTAGTATGATGATGATAGCAGAAAGGTTTTGTTAGACCAAGGT	1391	
DB	2066	AGTTAACTCAAAAAGATTAAATTTGGCAATGGATAGCTGAAAGATTGTAAAGAGGAAGA	2125	
QY	1392	TGGGATGACGACTAAGGATGTGC	1414	
DB	2126	AGGAAAAACATTAGAGCACCTCG	2148	

## RESULT 2

US-11-031-206-107  
; Sequence 107, Application US/11031206  
; Publication No. US2006003195A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni



US-11-031-206-107

Query Match 2.6%; Score 80.6; DB 9; Length 644;  
 Best Local Similarity 52.2%; Pred. No. 5.4e-11;  
 Matches 226; Conservative 0; Mismatches 201; Indels 6; Gaps 2;  
 QY 1123 CTACCATAGCAATCTTACATAGGAGCTGTGCTGCACTAAACAGGTGTGAGATGG 1182  
 DB 1. CTGCCACTAGCAATTTGACAGTCGGCAGCTTGTCTCATCTAGACCAAAATA-AAAT 59  
 QY 1183 GAGAAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAAACCAAGCTGGAAGCTTTG 1242  
 DB 60 TTGGAAATCAACATACACAGCTTCGGAGTGAGTTGTCAACCAA-----TGATCATGTC 114  
 QY 1243 AGGAGATGTGACCTTAGGTTCACACACCTACATCCCATTTGTAACCAATGCTTTTGG 1302  
 DB 115 CGAGCAATCTTAAATCTAAGCTACCATGATCTATCTGGAGATCTCAGAAAATGCTTCTTG 174  
 QY 1303 TATCTAAGTATCTTCTGAGGATTTTGAATCAAAAGAAATCGTCTAGTAGGTAGATGG 1362  
 DB 175 TATTGAGCTTGTCTGAGACTACCCATGTCAAGGAGCCCTTGTGCGGCTCTGG 234  
 QY 1363 ATAGCAGAGGGTTGTGTAGACCAAGGTGGGTGAGCAGCTAAGGATGTGCGAGAAAGT 1422  
 DB 235 GTCCGAGAGGTTTGTGTAGTAAAGAAAGAAATACACCANAGAGAGGTGGCTGAGGGA 294  
 QY 1423 TACTTTAATGAGCTAATCAACGAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGA 1482  
 DB 295 AATCTAGGAATGTATCCACCTGATATGCTTGAAGTTGTAGACTATGATGAGCTTGGC 354  
 QY 1483 AAAATTAGACTTGTGCAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGA 1542  
 DB 355 AGGTTAGCACTTGCAGATGATATCATGAGGACCTGGCACTTTGTGTGCCAAA 414  
 QY 1543 CAGGAAATTTTG 1555  
 DB 415 NAAGAGAGAGTTTG 427

RESULT 3

US-11-031-206-109  
 ; Sequence 109, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; CURRENT FILING DATE: 2005-01-07  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436

US-11-031-206-107  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 109  
 ; LENGTH: 1944  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; US-11-031-206-109

Query Match 2.6%; Score 79.8; DB 9; Length 1944;  
 Best Local Similarity 52.2%; Pred. No. 1.6e-10;  
 Matches 227; Conservative 0; Mismatches 202; Indels 6; Gaps 2;  
 QY 1121 GTCTACATAGCAATCTTACATAGGAGCTGTGCTTGGCACTAAACAGGTGTGAGAT 1180  
 DB 12 GCCTGCCACTAGCAATTTGTACAGTCGGCAGCTTGTCTCATCTAGACCAAAATA-AAC 70  
 QY 1181 GCGAGAAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAAACCAAGCTTGAAGCTT 1240  
 DB 71 ATTGGAAATCAACATACACAGCTTCGGAGTGAGTTGTCAACCAA-----TGATCATG 125  
 QY 1241 TGAGGAGAAATGGTGACCTTAGGTTCACACCACTACCATCCCATTTGAAACCATGCTTTT 1300  
 DB 126 TCCGAGCAATCTTAAATCTAAGCTACCATGATCTATCTGGAGATCTCAGAAAATGCTTCT 185  
 QY 1301 TGTATCTAAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360  
 DB 186 TGTATCTGAGCTTGTCTTCTGAGACTACCCCATGTACGGAAGCCCTTGTGCGGCTCT 245  
 QY 1361 GGATAGCAGAGGGTTTGTAGACCAAGGTGGGATGACACTAAGATGTGCGAGAAA 1420  
 DB 246 GGGTCGAGAGGTTTGTCTGAGTAAAGAAAGAAATACACCAAGAGGAGGTGGCTGAGG 305  
 QY 1421 GTTACTTTAATGAGCTAATCAACCAAGTATGATTCAAGCATCAAGGTGGGCATACGAG 1480  
 DB 306 GAAATCTCATGGAATGTACCCCATGTATGCTTGAAGTTGTAGACTATGATGAGCTTG 365  
 QY 1481 GAAAAATTAAGACTTGTGCAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGA 1540  
 DB 366 GCAGGGTTAGCACTTGCAGATGATATCATGAGGACCTGGCACTTTGTGTGCCA 425  
 QY 1541 GACAGGAAATTTTG 1555  
 DB 426 AAGAGAGAGTTTG 440

RESULT 4

US-11-031-206-137  
 ; Sequence 137, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; CURRENT FILING DATE: 2005-01-07  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436



```

; Publication No. US20060031959A1.
;
; GENERAL INFORMATION:
;
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
;
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
;
; TITLE OF INVENTION: Stress Response
;
; FILE REFERENCE: BB1357 US NA
;
; CURRENT FILING DATE: 2005-01-07
;
; CURRENT APPLICATION NUMBER: US/09/566,394
;
; PRIOR FILING DATE: 2000-05-05

```

```

RESULT 7
US-11-031-206-127
; Sequence 127, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response

```

```

/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: 60/133427
/ PRIOR FILING DATE: 1999-05-11
/ PRIOR APPLICATION NUMBER: 60/133437
/ PRIOR FILING DATE: 1999-05-11
/ PRIOR APPLICATION NUMBER: 60/133428
/ PRIOR FILING DATE: 1999-05-11
/ PRIOR APPLICATION NUMBER: 60/133438
/ PRIOR FILING DATE: 1999-05-11
/ PRIOR APPLICATION NUMBER: 60/133436
/ PRIOR FILING DATE: 1999-05-11
/ PRIOR APPLICATION NUMBER: 60/137667
/ PRIOR FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 208
/ SOFTWARE: Microsoft Office 97

```

```

, SEQ ID NO 123
,
, LENGTH: 306
,
, TYPE: DNA
,
, ORGANISM: Glycine max
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (3)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (146)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (156)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (172)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (179)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (219)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (257)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (272)
,
, FEATURE:
,
, NAME/KEY: unsure
,
, LOCATION: (290)

```

```

; NAME/KEY: unsure
; LOCATION: (294)
US-11-031-206-123
Query Match
2.2%; Score 67.8; DB 9; Length 306;

```

Db 533 ACAAGAGAGATTTTCAGAGTGAAGATGCGCGCTGATTTAGAGCCCTCGGTAGATCC 592  
Qy 1102 ATTGTAATAAATGTGCTCTACCAATTAGCAATCTTACAATAGGAGCTGTGCTTGA 1161  
Db 593 ATTGTGAACCTTTGTGGGGTTTACCACTTGCCATTGTGTTAGCAGGACTTGTGGC 652  
Qy 1162 ACTAAACAGGTGTGAGAAATCTATGAACACCTTCCTTCAGAACTAGAAATA 1221  
Db 653 AAGAAGAGAGTCAAGAGAGTGTCT--AGATCAAGGAGTGTGGCTTTA 710  
Qy 1222 AACCAAGCCTGGAAGCTTTGAGGAGATGTTGAGCCCTAGGTTACAACCACTTACATCC 1281  
Db 711 CACAGGATAAGAGTGAATGATATGCTGGAACCTTAGGTATGACAACTGCTGAA 770  
Qy 1282 CATTGGAACCATGCTTTTGTATCTAAGTATCTTCC 1319  
Db 771 AGATTATGCTTGTCTTTTGTATTTGTAATTTGGAATCTGTC 808

RESULT 8

US-11-031-206-139  
; Sequence 139, Application US/11031206  
; Publication No. US20060031959A1

GENERAL INFORMATION:

; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Jean T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

; FILE REFERENCE: B81357 US NA

; CURRENT APPLICATION NUMBER: US/11/031,206

; CURRENT FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: US/09/566,394

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: 60/133038

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133042

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133427

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133437

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133428

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133438

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133436

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/137667

; PRIOR FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 139

; LENGTH: 634

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (378)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (420)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (456)

; FEATURE:

; NAME/KEY: unsure  
; LOCATION: (495)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (498)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (506)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (546)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (561)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (567)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (577)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (581)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (583)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (599)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (615)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (621)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (623)  
US-11-031-206-139

Query Match

1.5%; Score 48; DB 9; Length 634;

Best Local Similarity 51.1%; Pred. No. 0.026;

Matches 142; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

Qy 1102 ATTGTAATAAATGTGCTCTACCAATTAGCAATCTTACAATAGGAGCTGTGCTTGA 1161

Db 3 ATAGTTGATAGGTGTCTACCTCTAGCAATTTGTACCAATTGTGCTGCAATGCTCT 62

Qy 1162 ACTAAACAGGTGTGAGAAATCTATGAACACCTTCCTTCAGAACTAGAAATA 1221

Db 63 TCAAGACAACGATTAGACATTTGGAAATCAAAAATACATCAGCTT-----CGAAGCGAG 116

Qy 1222 AACCCAGGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTAGGTTTACAACCACTTACATCC 1281

Db 117 TTGTCAAACAATGATCATGTCCGAGCAATTTTAAACCTGAGCTACCATGACCTTCCAGAC 176

Qy 1282 CATTGAAACCACTGCTTTTGTATCTAGTATCTTCTGAGGATTTGAAATCAAAAGG 1341

Db 177 GACCTCAAAACCTGTTTTTATCTAGTATCTTCTGAGGATTTGAAATCAAAAGG 1341

Qy 1342 AATCGTCTAGTAGTAGTATGATAGTACAGAGGCTTTGT 1379

Db 237 GAAACCTTGTGCGGCTGTGGGTTCGCCAAGGCTTGT 274

RESULT 9

US-11-031-206-135

; Sequence 135, Application US/11031206

; Publication No. US20060031959A1

; GENERAL INFORMATION:

; APPLICANT: Rafalski, Antoni

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Falco, Saverio Carl

```

; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: B1357 US NA
; CURRENT APPLICATION NUMBER: US/11/031,206
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 135
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (423)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (426)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (438)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (468)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (507) .. (508)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (514)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (569)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (582)
; US-11-031-206-135

Query Match 1.4%; Score 43; DB 9; Length 590;
Best Local Similarity 51.4%; Pred. No. 0.53;
Matches 125; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 1102 ATTGTAATAAATGCTGCTACCAATAGCAATCTTACCAATAGGAGCTGTGCTGCA 1161
Db 4 ATTTAAAAAAATGAGGCTTTTACCACTGGGATCAATGCCATATCCAGCTTGTGTCT 63
QY 1162 ACT---AAACAGGTGTGAGATGGGAGAAATCTATGACACCTTCTTTCAGACTAGAA 1218

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```

Db 64 ACTGGGAAAAAACAAGAGAGTGTATCAGGTTCCGAGCTCTATTGTTATGCGCAAGGA 123
QY 1219 ATAAACCAAGCCTGGAAGCTTTGAGGAGAAATGGTGACCTAGGTTTACAAACCACTACCA 1278
Db 124 AAAAATTCACATTCATGATCCATGATTAATATATCTTTCAGGTTATTTGACCTCC 183
QY 1279 TCCCATTTGAAACCATGCTTTTGTATCTATCAATGATCTTTTCTGAGATTTTGAATCAA 1338
Db 184 CATCACCTAAGATATTGCTTATTTGACTATGTTTCTTGAAGATTATCGGGTTGAA 243
QY 1339 AGG 1341
Db 244 ATG 246

RESULT 10
US-09-925-065A-284566
; Sequence 284566, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284566
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-284566

Query Match 1.3%; Score 41; DB 6; Length 879;
Best Local Similarity 52.7%; Pred. No. 2.2;
Matches 89; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1001 TCTTGCAGATGAACGATGCCATTAACATTCCTACTCAGAAACAAATTAATCATGAAG 1060
Db 671 TCCGAAATTAAGGAGAGATTAACATCTTAAAGAAATCAATCAGAGATTTGGAAT 730
QY 1061 ACATGGAAATCAATAAAATATGCAAAAGATGGTTGAAACGAAATGTTAAATTAATGTGTC 1120
Db 731 TGAAGAACTCACAATAAAAGTTTAAATAACAATGAAAGTTCTGTAATAGACTGGACC 790
QY 1121 GTCTACCATTAAGCAATACCTTACAATAGGAGCTGTGCTTGGCACTAAACA 1169
Db 791 AAGCAATTAAGGAGTTTCAGAGCTTGAACATGATCTTTCAACTAACA 839

RESULT 11
US-11-031-206-117
; Sequence 117, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.

```

```
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BBI357 US NA
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 117
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Oryza sativa
US-11-031-206-117
```

```
Query Match 1.3%; Score 40.8; DB 9; Length 507;
Best Local Similarity 51.7%; Pred. No. 1.9;
Matches 93; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1209 AGACTGAAATTAACCCAGCTGGAGCTTTGAGGAGATGGTGACCTAGGTTACAA 1268
Db 115 AGATGGGATTAACAACTGGTGACATGATATATGCCAGCATTAAGCTTACATGA 174

QY 1269 CCACCTACCTCCATTTGAACATGCTTTTGTATCTAATGATCTTTCTGAGGATTT 1328
Db 175 CTATCTCCCTTCCATCTGCAACAATGTTTATATATTTGCTTTGTTCTGAGATTA 234

QY 1329 TCAATCAAAAGGATCTCTAGTAGTAGATGATAGCAGAGGTTTGTAGACCAAA 1388
Db 235 CAGTTTGACAGTGAAGTTGATTCACCTATGATGAGCTAGACATTTTACATCA 294
```

```
RESULT 12
US-09-925-065A-284567
; Sequence 284567, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 284567
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-284568
```

```
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 284567
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-284567

Query Match 1.3%; Score 40.6; DB 6; Length 469;
Best Local Similarity 52.1%; Pred. No. 2.1;
Matches 88; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

QY 1001 TCTTGCAGATGAACGATGCGCATTAACATTCCTACTCAGAGAAAACAATAAATCATGAG 1060
Db 261 TCCAGAAAATAAAGGAGAGATAAACAATCTTTAAAAAGAAATCAATCAGAGATTTCTGGAAT 320

QY 1061 ACATGGAATCAAAATAAATAATATGCAAAAGATGGTTGAACGAAATGTTAAATAAATGTGTC 1120
Db 321 TGAATAACTCACATTAATAAGTTTAAATAACAAATTTGAAGTTCTGTAATAGACTGGACC 380

QY 1121 GTTACCATTAAGCAATTAATCAATAGGAGCTGTGCTTGGCACTAAACA 1169
Db 381 AAGCAGAATAAGGAGTTTCAGAGCTTGAACCTGATCTTTCAAACTAACA 429
```

```
RESULT 13
US-09-925-065A-284568
; Sequence 284568, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 284568
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-284568
```

```
Query Match 1.3%; Score 40.6; DB 6; Length 469;
Best Local Similarity 52.1%; Pred. No. 2.1;
Matches 88; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

QY 1001 TCTTGCAGATGAACGATGCGCATTAACATTCCTACTCAGAGAAAACAATAAATCATGAG 1060
Db 261 TCCAGAAAATAAAGGAGAGATAAACAATCTTTAAAAAGAAATCAATCAGAGATTTCTGGAAT 320

QY 1061 ACATGGAATCAAAATAAATAATATGCAAAAGATGGTTGAACGAAATGTTAAATAAATGTGTC 1120
Db 321 TGAATAACTCACATTAATAAGTTTAAATAACAAATTTGAAGTTCTGTAATAGACTGGACC 380

QY 1121 GTTACCATTAAGCAATTAATCAATAGGAGCTGTGCTTGGCACTAAACA 1169
Db 381 AAGCAGAATAAGGAGTTTCAGAGCTTGAACCTGATCTTTCAAACTAACA 429
```

```
RESULT 14
US-09-925-065A-107964/c
; Sequence 107964, Application US/09925065A
```

```
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107964
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-107964

Query Match      1.3%; Score 40.2; DB 6; Length 625;
Best Local Similarity 49.4%; Pred. No. 3.1;
Matches 131; Conservative 0; Mismatches 133; Indels 1; Gaps 1;

QY      828 GAAGAGGTACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGATTGGATAAA 887
DB      593 GAGCAGAAAATCTCAATCTCATGTTAAATATGACTCTTGAAAACCTACAAAAGTTGCAAGGA 534
QY      888 TGAATTGCAATTTCTTAAGAACAAATGAAGGGCAGTCGAATAGTAATAACCACTCGGAA 947
DB      533 AGGATATGTAATAGGGAGATACATTTAGAAAAGTAATTTGAAGATAGATTATGAAGCTCCA 474
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Job time : 897 secs

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; Sequence 107965, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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GenCore version 5.1.7  
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OM protein - nucleic search, **FASTX**  
Run on: March 9, 2006, 21:39:16 ; Search time 423 Seconds  
(without alignments)  
4336.746 Million cell updates/sec

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Perfect score: 5268  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	975.5	18.5	10322	3	US-09-330-330-3
3	637.5	12.1	5222	3	US-09-336-948B-68
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5	637.5	12.1	5696	3	US-09-993-170-60
6	618	11.7	3099	3	US-09-360-186-2
7	618	11.7	3099	3	US-09-864-680A-2
8	614	11.7	31491	3	US-09-360-186-1
9	614	11.7	31491	3	US-09-864-680A-1

10	609.5	11.6	2718	3	US-09-360-186-4	Sequence 4, Appli
11	609.5	11.6	2718	3	US-09-864-680A-4	Sequence 4, Appli
12	607.5	11.5	4465	3	US-08-930-996A-3	Sequence 3, Appli
13	602	11.4	4208	3	US-09-004-838-1	Sequence 1, Appli
14	594.5	11.3	4163	3	US-09-004-838-70	Sequence 70, Appli
15	580.5	11.0	4946	3	US-08-930-996A-1	Sequence 1, Appli
16	572	10.9	3741	3	US-08-803-286A-1	Sequence 1, Appli
17	564	10.7	5475	2	US-08-680-327-1	Sequence 1, Appli
18	557	10.6	5475	2	US-08-228-246-3	Sequence 3, Appli
19	557	10.6	9870	3	US-09-245-928A-15	Sequence 15, Appli
20	552	10.5	51952	3	US-08-947-823-1	Sequence 1, Appli
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27	514.5	9.8	5134	3	US-09-301-085-157	Sequence 157, App
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36	405.5	7.7	2903	6	PCT-US95-04589-1	Sequence 1, Appli
37	405.5	7.2	2903	6	PCT-US95-04589-1	Sequence 141, App
38	378.5	7.2	3432	3	US-08-310-912A-141	Sequence 141, App
39	378.5	7.2	3432	3	US-09-301-085-141	Sequence 141, App
40	378.5	7.2	3432	6	PCT-US95-04589-141	Sequence 141, App
41	362	6.9	4211	3	US-09-004-838-106	Sequence 106, App
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43	332	6.3	3756	2	US-08-261-663A-2	Sequence 2, Appli
44	332	6.3	3760	3	US-09-357-206A-2	Sequence 2, Appli
45	332	6.3	3760	6	PCT-US95-07754A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-330-330-2  
; Sequence 2, Application US/09330330  
; Patent No. 6274789

GENERAL INFORMATION:

APPLICANT: Yano, Masahiro  
APPLICANT: Iwamoto, Masao  
APPLICANT: Katayose, Yuichi  
APPLICANT: Sasaki, Takuji  
APPLICANT: Wang, Zi-Xuan  
APPLICANT: Yamanouchi, Utako  
APPLICANT: Iehimaru, Lisa

TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,330

FILING DATE: 11-JUN-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 10-181455

FILING DATE: 12-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Ph.D., J.D., Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 06501/032001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3925 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 82...3696  
US-09-330-330-2

Alignment Scores:  
Pred. No.: 3 29e-123 Length: 3925  
Score: 1182.00 Matches: 354  
Percent Similarity: 43.2% Conservative: 197  
Best Local Similarity: 27.7% Mismatches: 376  
Query Match: 22.4% Indels: 349  
Dbs: 3 Gaps: 36

US-10-656-394A-8 (1-1032) x US-09-330-330-2 (1-3925)

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Db 2788 GCCCTAGCCGCGGTGATGCGTGACTTTCGCTTGGTGGGTGAAATTCACATCTATCATG 2847  
Qy 711 -----GluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAsp 726  
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Qy 921 GlyIleHisLeuProLysLeuLysGluIleProIleArg-TyrGlySerLysValAl 940  
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Qy 960 cTyrSerAspArgArgTyrHisAspLeuGlyAla-----GluAl 973  
Db 3595 GCTGGGAGAGAGGTACAGGAGCAGGCGCAAGGAGGTGCACTGAAGAGGAAATC 3654  
Qy 973 aGluGlySerSerIleGluValGlnThrAlaAspProValProAsp 988  
Db 3655 CGAGAACAGCTTGTCTCGGAATCCAAACCAACCATCATCTACCTGAG 3700

## RESULT 2

US-09-330-330-3  
; Sequence 3, Application US/09330330  
; Patent No. 6274789  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Masahiro  
; APPLICANT: Iwamoto, Masao  
; APPLICANT: Katayose, Yuichi

APPLICANT: Sasaki, Takuji  
 APPLICANT: Wang, Zi-Xuan  
 APPLICANT: Yamanouchi, Utako  
 APPLICANT: Ishimaru, Lisa  
 TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/330,330  
 FILING DATE: 11-JUN-1999  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP-10-181455  
 FILING DATE: 12-JUN-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Ph.D., J.D., Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 06501/032001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10322 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 US-09-330-330-3

Alignment Scores:  
 Pred. No.: 6,54e-99 Length: 10322  
 Score: 975.50 Matches: 319  
 Percent Similarity: 45.2% Conservative: 181  
 Best Local Similarity: 28.9% Mismatches: 372  
 Query Match: 18.5% Indels: 235  
 DB: 3 Gaps: 36

US-10-656-394A-8 (1-1032) x US-09-330-330-3 (1-10322)

Qy	163	LeuValGlyPheSerAspSerLysArgLeuLeuMetIleAspThrAsnAlaAsn	182
Db	6119	CTTATTGGCGGAGAGAAATAATATCGAAATAACACACTTAATT---TTAAACAATGAT	6175
Qy	183	AspGlyProAlaIleValIleCysValValGlyMetGlyGlyLeuGlyValThrAlaLeu	202
Db	6176	AGCCAGCAGGTTTCAGGTGATCTCTGTGGGGAATGGTGGCTTGGAAATACCCCTA	6235
Qy	203	SerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAlaTrp	222
Db	6236	GTAAGCGGTGTTTATCAAGGCCAAGG---CTGAGTGATAAGTTTGCACAGTAGTGT	6292
Qy	223	IleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeu	242
Db	6293	GTCAACATCATCGGTCCTTTCATCTCTGTAGAGCTCTTAGGAGTTGGTGAGCACA	6352
Qy	243	LeuGlyProSerSerLeuAspGlnLeuGln-----GluLeuGlnGly	257
Db	6353	CATAAAGGATCTTCTAAGAGGAGAACTGTAGAAAATAGAGTCAGCAGTAGAAGAAC	6412
Qy	258	LysValValGlnValHisHisLeuSerGluTyrlleuIleGluLeuLysGluLys	277
Db	6413	CTAGCATCGATGGAGGATACCGAGTTGACTGGCGAGTTGAAAAGGCTTTTAGAAGA	6472
Qy	278	ArgTyrPheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGlu	297
Db	6473	AGTTGCTTGTGTTCTTAGATGATTTCTCAGATACCTCAGATGGGACGACATAAACCA	6532
Qy	298	IleAlaPheProLysAsnAsnLysLysGlySerArgIleValIleThrArgAsnVal	317
Db	6533	ACGTTATTCCCTCTG---TTGGAAAGACAAAGCCGAAATTAATGTGACTACAGAAAG	6589
Qy	318	AspLeuAlaGluLysCysAlaThrAlaSer---LeuValTyrHisLeuAspPheLeuGln	336
Db	6590	AATATTGCCAACCATTTGCTCAGCGMAAATGGAATGTGCACACCTTAAGTCTTAA	6649
Qy	337	MetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsn-----	349
Db	6650	CATAATGATGCAATTTGCTCTTGGTGGAGAGGT-ATATATAAGTGTGCTCCATTTTCT	6708
Qy	349	-----	349
Db	6709	TGCTTTTGATATCTTTTAATCAATTGAGTTTATCCAAATCAAGATGATATTGTGTCAG	6768
Qy	349	-----	349
Db	6769	AAATAGCATATCTAGATTATATACAACTTAATCTGTTCTCACAAATAGCAATGCAG	6828
Qy	349	-----	349
Db	6829	TTCTTAATATGACCTGCATTGGATGGACGTTAGATGTGACTTTGTTTGTATGTAATGG	6888
Qy	349	-----	349
Db	6889	TGGCCTTCATCTTCATTGTTTAAATAGTAAAGACGTATTCTTAAATTTTATTTTGTGT	6948
Qy	350	-----LysAsn	351
Db	6949	TTACTTTTAGACCAATAAAGCTTAATTTCTATCAATGTGCTGAGTATTTCGAGGAGCTACA	7008
Qy	352	HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys	371
Db	7009	TATTTGGATGATCAGAACCAATCCAGAGTTGGTTAAAGAACGAAAAAATAATCTTAAAG	7068
Qy	372	CysGlyArgLeuProLeuAlaIleLeuThrIleGlyValAlaValLeuAlaThr-----Lys	389
Db	7069	TGCGATGAGTCCCTTCGCAATAGTGTGCATAGTGGATTCTTGGCAACCGACCAAG	7128
Qy	390	GlnValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuLeuLeuAsnPro	409
Db	7129	ACCCAGAGAGTGGAGAAAAATTTGAACGAGAAATATCAATGCTGAGTTGGAATGAATCCA	7188

Qy	86	PheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArg	105
Db	5760	TTCAAAATAGGATCCAAATAGGTTTATATAGTCTGCAATTAATGAAGGAATTAT	5819
Qy	106	HisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGluGluVal-----	122
Db	5820	CATTATGTTGTTGTTATCTTTCATGACCG-AAAAACAAGGCTAAACACTATCATGTATGA	5878
Qy	123	-----SerSerArgAsnThrArgTyrSerLeu-----	131
Db	5879	AAATTTAAGCTAAAGTTGTTCTTAATCATTTGCTCCCTTTGTTAGGGTCCCAATTT	5938
Qy	132	-----ValLysProLysSer-----	136
Db	5939	ATAGAGGATTCAGTGAAGCCAGTGTCTATCTCGGATGTGCCATCAAGTACAAACAAT	5998
Qy	137	-----SerGlyThrGluIleAsp-----MetAspSerTyrAlaGluAsp	149
Db	5999	CATACAGTGGCCCGTGGTGCAGATTATAGATCATCAATGATGCTGATGAGAGAAG	6058
Qy	150	IleArgAsnGlnSerAlaArgAsnVal-----AspGluAlaGlu	162
Db	6059	GTGCTAGAAAGAGTCTTACTCGCATTAGGACAAGTGTGTTGCTTTCGAGGAATCACA	6118

410 SerLeuGluAlaLeuArgArgMetValThrLeuGlyTyAsnHisLeuProSerHisLeu 429  
Db GAGCTTGGATGATGAAGAACCGCTCTTGAAGAAAGCTATGATGGTTTACCATACCATCTC 7248  
430 LysProCysPheLeuTyLeuSerIlePheProGluAspPheGluIleLysArgAsnArg 449  
Db AGTCATGTTTTTATATCTGCTGCTATTTTCCCTGGAAGACAGATCATTTAGTTCGAAGGCT 7308  
450 LeuValGlyArgTTPilleAlaGluGlyPheValArgProLysValGlyMetThrThrLys 469  
Db TTTGGTGCATCGTTGGCGACGAGAAAGTTACTCAACTCGACGACATGGGAAATCTGCCATT 7368  
470 AspValGlyGluSerTyPheAsnGluLeuIleAsnArgSerMetIle 486  
Db GAAATGCTAACCGCTACTTTCATCGAACTCAAGNATGAGAGCATGATTTTACCATTCCAG 7428  
487 ArgSerArgValGlyIleAlaGlyLys---IleLysThrCysArgIleHisAspIle 505  
Db CAATCA-----GGTAGCAGGAGAAATCAATTTGACTCTTGCAGAACTCATGATCTCATG 7482  
506 ArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAsp 525  
Db CGTGATCTCCCTCTCAAGTCAACGAGGAAACCTGTTTATAGGTGAGGAGGAGGC 7542  
526 GlySerAspLeuValGlnGluAsnThrArgHisIleAla-----PheHisGly 541  
Db TGCAGCGCTACATACATGCTGCAATTCGTATCTGCTATGATGAGTCACTTGGAGGGA 7602  
542 SerMetSerCysLeuThrGlyLeu---AspTrpSerIleIleArgSerLeuAlaIlePhe 560  
Db GATAAGATGAATTCAGCGGATAGTGGACTGCTCGGATACGATCGTTATCTGTTT 7662  
561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db GGGGATTTGAAGCAATTTTGTGTTTATGAGG-----AAGATGAGGTTTATACGA 7710  
581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db GTGCTGACTTTGAAGG---ACTAGAGGCTAGNATATCATCACCTTCATGATTTGG 7767  
601 LeuLysCysHisLeuLysLeuSerIleGlyTySerSerSerIleTySerLeuPro 620  
Db AAGCTTAATCACCTAAATCTCTTCTCTAGAGGATGCTATGATGATGATCTATGCA 7827  
621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIleAla 640  
Db GATTACTGGCAACCTCAGGCACTCCAGATGCTAGACATCAGAGGTACATATGATAAG 7887  
641 AlaLeuProSer-----GluLeuSerLysLeuGlnCysLeuHisThrLeuArgCys 657  
Db GCTTTTCCAAAACCATCATCAAGCTTCAGAGCTCAGTACATTCATCTCGGCGCAAA 7947  
658 IleGlyGlnPheHisTyAspAsnPheSerLeuAsnHisProMetLys-----Cys 674  
Db ACAGATGATGATGGGAGGAAAGCATAGTTTATGAGAGGCTGCTGTAAGGCTGGATGT 8007  
675 IleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspArg 694  
Db ATATGTGCAACATGTTGCTCTCTCTT-----GluSerIleGlyValLysVal 717  
695 AlaLysGlnIleAlaGluLeuHis-----MetAlaThrLysSerCysTrpSer 710  
Db TGGCAATATGATGGCCCTCTCCATGAAGCCCTAGCCGGCTGATCGTGGACTTTCGT 8097  
711 -----GluSerIleGlyValLysVal 717  
8098 TGCTGCGTGAATTCCTCATCTATCATGACGGAGTACATGAGAGGAGGCGCTATGTTG 8157  
718 ProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyValAspIleArgArg 737  
Db CCAAGTGGGATTAGAAAACCTGAAGACTTGCACACACTAGGAGAACATAAATGTCGAAGG 8217  
738 ThrSerSerArgAlaTlLeuGluLeuGlnGlnLeuSerLysLeuArgLysLeuGlyVal 757

TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-336-946B-68

## Alignment Scores:

Pred. No.: 6,48e-61 Length: 5222  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-336-946B-68 (1-5222)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 2426 ATGGCGCGCGGTCATTCATCGCAGGCGTTCATCATCGCGTCCCTGACGACGACGCTC 2485  
Qy 21 AlaSer-----AlaAlaAlaAspGluThrSerLeuLeu 31  
Db 2486 GACTCGCTGCTGCGAGCGCGCGGAGCGCGCGCTGCGCAACGCTGCTCGCTCGCG 2545  
Qy 32 LeuGlyValGluLysAspIleTyrIleLysAspGluLeuLysThrMet-----Gln 49  
Db 2546 AAGGGGAGAGGAGAGAGTCTCTCTCAGAGCGGATCTCCGACACCTGCTAGATGAC 2605  
Qy 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysAspGluLeuLys 66  
Db 2606 TACTACCTCTGCTGAGCGCGCTGACACCGCGCCAGCGCGAGCTCGACGGCGCG 2665  
Qy 67 ValTyrAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
Db 2666 TGCTGGGCTAAGGAGGTTCGCGAGCTCTCTACGACGTCGACGACTTCTTCGACGACTA 2725  
Qy 87 LysValHisIle----- 90  
Db 2726 ACGACCCAGCTCTCCACACCGCGCGCGCGATGCGAGTACGCTGCTGTCGCAAG 2785  
Qy 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
Db 2786 AAGATGATCAGCAGCATGATCGCGCGCTTCGAGGGGAGCTTAACCGCGCGCGTGGATC 2845  
Qy 109 AlaIleArgIleHisAsnLeuLysSerArgValGluGluValSerSerArgAsnThrArg 128  
Db 2846 GCGCAGGAGTCACTGTTTACGGCGCGCGTGAAGAGGACCATTCGCCGCCACGAGAGC 2905  
Qy 129 TyrSerLeuValLysProIleSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148  
Db 2906 TACCATCTTGGCAGGCGCACCTCGAGCTCGAGCGCGGAGGAGGAGGAGGAGGAGGAGG 2959  
Qy 149 AspIleArgAsnGlnSerAlaArgAsn----- 157  
Db 2960 GACGATCGCGAGGACTCCGCGCGCAAGCGCGCGGTTCTGTCGCTGACGTTGCGG 3019  
Qy 158 ValAspGluAla-----GluLeuValGlyPheSerAspSerLysLysArgLeu 173  
Db 3020 ATGACGACGCTGCTGTGACGCGCGAGCTGCTGTGAGGATATTCGATGCAAAAGCTC 3079  
Qy 174 LeuGluMetIleAspThrAsnAlaAsnAspGlyPro-----AlaLysValIleCysValVal 192  
Db 3080 GTCCGGTGGCTG-----GCCGACGCGCGAGCGGAGCTCAAGTGGCTTCCATTGTT 3130  
Qy 193 GlyMetGlyClyLeuGlyThrAlaLeuSerArgLysIlePheGluSerGlu-----Glu 211  
Db 3131 GGATCCGAGGTCTGGCAGAGCAGCGCTGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 3190  
Qy 212 AspIleArgLysAsnPheProCysAsnAlaTyrIleThrValSerGlnSerPheHisArg 231  
Db 3191 CGGTTGATCGCGGTTTCTGACTCGCGGCTTTCGTCGCGAGCGCGCGAGCGCTGACATG 3250  
Qy 232 IleGluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeu 251  
Db 3251 ACGAAGATCTCTACCGACATGCTGTGCACAGCTG-----CGGCCA 3289

Qy 252 LeuGlnGluLeuGlnGlyLysValValValGlnValHisLeuSerGluTyrLeuIle 271  
Db 3290 CAACATCAGCATCAGTCTTGGGAGGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3349  
Qy 272 GluGluLeuLysGlyLysArgTyrPheValValLeuLeuAspAspLeuTyrIleLeuHisAsp 291  
Db 3350 ACCGATTTGCAAGATTAAGGCTACTTCATCATTAATGAAGATTTATGGGCTTCATCAATG 3409  
Qy 292 TyrAsnTyrIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
Db 3410 TGGGATATTGTTAGCCGT---GGTTCGCTGATAATAAT---AGTTCGATAGAACTA 3463  
Qy 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
Db 3464 ATAACAACAGAAATGAACCTGAGCTTGGCATGCTGTGGATATAACTCAGAGCACATT 3523  
Qy 332 LeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351  
Db 3524 ATTAAGATTGATCCCACTGGGTGATGTCCTCAAGTCAATTTGTTTCAGTGGAGTTGTT 3583  
Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
Db 3584 GGCCAGGAATGAATTCCTGGACATCTTCTGAGCTTCTCATGACATGATAAATAA 3643  
Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnVal 391  
Db 3644 TGTGGTGGCTTCCCACTAGCAATA---ACTATAACAGCCAGACATTTTAAAGCCAGCTG 3700  
Qy 392 SerGluTyrGluLysPheTyrGluHisLeu-----ProSerGluLeuGlu 406  
Db 3701 TTAGATGAGATCCCAATGAATCATACATAAATCATGACTTCTTCCATTTGAAG 3760  
Qy 407 IleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuPro 426  
Db 3761 AAAAACTCTACTTTCGAGGATGAGGAGTACTCAACCTTATTTACATAATATCTCT 3820  
Qy 427 SerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLys 446  
Db 3821 CATTTGTTGAAAGCATGCTGTTATACCTTAGCATCTCAAGAGGACTACATAATAGG 3880  
Qy 447 ArgAsnArgLeuValGlyArgTyrIleAlaGluGlyPheValArgProLysValGlyMet 466  
Db 3881 AAGGCCAACTTGGTGGGCAATGATGGCTGCAAGTTTCAATTCATAGATAAATAA 3940  
Qy 467 ThrThrLysAspValGlyLysTyrPheAsnGluLeuIleAsnArgSerMetIleGln 486  
Db 3941 GTCATGGAAGAAGTTGCGAGGAATATTTGATGAACTTGTGTTAGGAGGCTGCTGCTCAA 4000  
Qy 487 ArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleArg 506  
Db 4001 CCAGTAGATGTTAACTGCAAAATGAGGTATTGTGATGTGATGACACCATGTTATTA 4060  
Qy 507 AspIleThrValSerIleSerArgGluAsnAspPhe-----ValLeuLeuProMetGlyAsp 525  
Db 4061 AATTCATCAGGTGTAAGTCAATAGAGGAATTTAGCAATTCATTCATTCATTCATTCAG 4120  
Qy 526 GlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCys 545  
Db 4121 ACACAGTAAGACATGCTGACAGGTTCCGCGACTTCGCTTCACTTCAGCAATGCACAT 4180  
Qy 546 LysThr-----GlyLeuAspTyrSerIleIleArgSerLeuAlaIlePheGly 561  
Db 4181 GATACACACCACTAGCAGGTTTGGAGCTCTCAAGTTCGATCGATGGCATTTTTCGGA 4240  
Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeu-----ArgMet 578  
Db 4241 -----CAAGTCAAGTGTATGCTTCCATTCAGATTATAGGCTT 4279  
Qy 579 LeuArgValLeu-----AspLeuGluAspValThrPheLeuIleThr 592  
Db 4280 TTTCCGAGTTCTGATCTTTGTTTGGCTGATCAGAGAAACAAAGCTAT----- 4330

QY 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612  
DB 4331 -----GACCTCACAGCATTTTGAACATGTTACAACTGAGATATCTGAAGATAACAGGT 4384  
QY 613 SerSerIleTyrSerLeuProArgSerIleGlyLeuGlnGlyLeuGlnThrLeu 632  
DB 4385 AATATCACAGTT---AAACTTCCAGAGAGATCCAGGACTACACACTTGCAGACATG 4441  
QY 633 AsnMetProSerThrTyrIleAlaLeuProSerGluSerIleSerLysLeuGlnCysLeu 652  
DB 4442 GAAGCAGATGCAAGAGCAACTGCTGCTCA---TTGGATATTGTTATACACAGTGTG 4498  
QY 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672  
DB 4499 TTGCACCTTCGCTTGTGA----- 4516  
QY 673 LysCysIleThrAsnThrIle-----CysLeuProLysValPheThrProLeuValSer 690  
DB 4517 -----CTACTTGATCTGCTCCCTCACTGTCCAGGTACATCTTCACC----- 4558  
QY 691 ArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSer 710  
DB 4558 ----- 4559  
QY 711 GluSerIleCysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeu 730  
DB 4559 -----AGCATCCCAATGAGTGGAAAGCTCAACAATCTCCGCAATTTA 4603  
QY 731 GluTyrValAspIleArgThrSerSerArgAlaIleLysGluLeuGlnLeuSer 750  
DB 4604 AACATT-----CCAGTCATGCAAAATTTCCAC----- 4630  
QY 751 LysLeuArgLysLeuGlyValThrAsnGlySerThrLysGluLysCysLysIleLeu 770  
DB 4630 ----- 4631  
QY 771 TyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyIle 790  
DB 4630 ----- 4631  
QY 791 SerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArg 810  
DB 4631 GATGACCTTGACACTCTCAAGGACTGGGATCTCTCACTGCTCTTCCTGCTGTTGCA 4690  
QY 811 ThrLeuValLeuAspGlyIleLeuGluMetProAsnTrpIleGluGlnLeuThrHis 830  
DB 4691 ACAGCGCTCGCGCAAGAATCGTC----- 4714  
QY 831 LeuLysAlaIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
DB 4715 -----CTCGGATGAGGG-----TTC 4732  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870  
DB 4733 GGGTCTCTCAAGTACTTCACTGTTTGTCT-----TGTACAGCACCATGTC 4774  
QY 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
DB 4775 ATGCTTTTGTGAAGAGCAATGCCGAGTGTGCAAGGTTA----- 4816  
QY 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
DB 4817 -----AATCAAGGTTCAATGCCAACGAGTTCAAG----- 4846  
QY 911 GlyGluCysArgLeuSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
DB 4847 -----CAGTATGACTCTAAGGAGACAGGTTGGACACTTGTGCGCTTCGAGAG 4897  
QY 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
DB 4898 ATCTCTCAAGAAATTTGGGGCACTGATGATGATGAATCAACAACTGAAGTGGAGTCT 4957  
QY 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963

DB 4958 GCCTTGAGGACTGCATTTCCAGCATCCGACCCGAGCAGCTTTATGGTT-----GAT 5011  
QY 964 ArgArgTyrHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGlnThrAla 983  
DB 5012 ATACAATGGGTGGATTGGATCTTTGGTCTGTGAAGGAGAGACTTGGATGAAGATTGGCA 5071  
RESULT 4  
US-09-993-170-57  
; Sequence 57, Application US/09993170  
; Patent No. 6743969  
; GENERAL INFORMATION:  
; APPLICANT: Valent, Barbara  
; APPLICANT: Bryan, Gregory  
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
; TITLE OF INVENTION: Specificity and Method for Engineering Altered  
; TITLE OF INVENTION: Specificity  
; FILE REFERENCE: BB1385 US NA  
; CURRENT APPLICATION NUMBER: US/09/993,170  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/248,335  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 57  
; LENGTH: 5222  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-993-170-57  
Alignment Scores:  
Pred. No.: 6,48e-61 Length: 5222  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-993-170-57 (1-5222)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
DB 2426 ATGGCGCCGCGGTCATTGTCATCGAGGGTGTTCATCATGCGTCCCTGACGAGCAAGCTC 2485  
QY 21 AlaSer-----AlaAlaAlaAspGluThrSerLeuLeu 31  
DB 2486 GACTCGCTGCTGTCGACCGCCGCGGCTGCGCAACCGTCTGCTGCTGCGG 2545  
QY 32 LeuGlyValGluLysAspIleTrpTyrIleLysAspGluLeuLysThrMet-----Gln 49  
DB 2546 AAGGGGAGAGAGAGAGAGATCTCTCTCTCAGAGGGCATCTCCGACACCTGTAGATGAC 2605  
QY 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysAspGluLeuLeuLys 66  
DB 2606 TACTACCTCTCTGTCGAGCCCGCTCAGACACCGCCGCGGAGCTTAACCGCGCGGTGATC 2665  
QY 67 ValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
DB 2666 TCGTGGCTTAAGGAGTTCGCGAGCTCTCTCTACGCTCGACGACTTCTCTCGACGAGCTA 2725  
QY 87 LysValHisIle----- 90  
DB 2726 ACGACCCAGCTCTCTCCACCGCGCGGCGGATGTCAGTAGTACACTGCTGTGTCAG 2785  
QY 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
DB 2786 AAGATGATCAGCAGCATGATCGCGGCTTCGAGGGGAGCTTAACCGCGCGGTGATC 2845  
QY 109 AlaIleArgIleHisAsnLeuLysSerArgValGluValSerSerArgAsnThrArg 128  
DB 2846 GCCGACGAGGTTCACCTCTTTCAGGGCGCGGTGAAGGAGGCCCATTCGCCGCCACGAGAC 2905  
QY 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148





QY 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
Db 4715 -----GCTCGGAATGAGGG-----TTC 4732  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyLys 870  
Db 4733 GGGTCTCTCAAGTACTTCATCTTGTTC-----TGTACACACATGC 4774  
QY 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
Db 4775 ATGACTTTTGTGGAAGAGCAATGCCGAGTGTGCAAGGTTA-----4816  
QY 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluLe 910  
Db 4817 -----AATCTAAGGTTCAATGCCAACGAGTTCAG-----4846  
QY 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
Db 4847 -----CAGTATGACTTAAGGACAGAGGTTGGAACACTTGGTCCCTTGCAGAG 4897  
QY 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
Db 4898 ATCTCTCAAGAATTTGGGGGCACTGATGATGAATCAACAACAACTCAAGTGGAGTCT 4957  
QY 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963  
Db 4958 GCCTTGAGACTGCAATTCGACAGATCCGACGCGGAGCACTCTTATGTT-----GAT 5011  
QY 964 ArgArgTyrHisAspLeuGlyAlaGluGlySerSerIleGluValGlnThrAla 983  
Db 5012 ATACAATGGTGGATTTGATCTTTGGTCTCAGGAGAGACTTGGATGAAGATTGGCA 5071

## RESULT 5

US-09-993-170-60  
; Sequence 60, Application US/09993170  
; Patent No. 6743969  
; GENERAL INFORMATION:  
; APPLICANT: Valant, Barbara  
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
; TITLE OF INVENTION: Specificity and Method for Engineering Altered  
; TITLE OF INVENTION: Specificity  
; FILE REFERENCE: BH1385 US NA  
; CURRENT APPLICATION NUMBER: US/09/993,170  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/248,335  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 60  
; LENGTH: 5696  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric Gene  
US-09-993-170-60

Alignment Scores:  
Pred. No.: 7.58e-61 Length: 5696  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-993-170-60 (1-5696)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 2426 ATGGCGCGCGGTCAATTCATCGCAGGAGTGTGTCATCGGTCCCTGACGACGAAGCTC 2485  
QY 21 AlaSer-----AlaAlaAlaAspGluThrSerLeuLeu 31

Db 2486 GACTCGTGTGTGTCAGCCGCGAGCCGCCGCCCTCGCGCAACCGTGTGCTGCGG 2545  
QY 32 LeuGlyValGluLysAspIleTyrTyrIleLysAspGluLeuLysThrMet-----Gln 49  
Db 2546 AAGGGGAGAGAGAAAGATCTCTCTCTCAGAGGCGATCTCCGACACCTGTAGATGAC 2605  
QY 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysLysAspGluLeuLys 66  
Db 2606 TACTACCTCTCTGTCGAGCCCGCTCAGACACCGCCCAACCGCCAGCTCGACGGGGG 2665  
QY 67 ValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
Db 2666 TCGTGGCTAAGGAGGTTTCGAGCTCTCTACGACGTTCGACGACTCTCTCGACGACTA 2725  
QY 87 LysValHisIle-----90  
Db 2726 ACGACCCAGCTCTCCACACCGCGCGCGGCGATGCGAGTAGCTGCTGTCGCAAG 2785  
QY 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
Db 2786 AGATGATCAGCAGCATGATCGCGCGCTTCGAGGGAGCTTAACCGCGCGGTGATC 2845  
QY 109 AlaIleArgIleHisAsnLeuLysSerArgValGluValSerSerArgAsnThrArg 128  
Db 2846 GCCGACGAGTCACTTTCAGGGCCCGCTGAAGAGGCCATTCGCCGCCACGAGAGC 2905  
QY 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148  
Db 2906 TACCATCTTGGCAGCGCACCTCGAGTTCGAGGCCGAGAGAGAACGACGAC-----GAC 2959  
QY 149 AspIleArgAsnGlnSerAlaArgAsn-----157  
Db 2960 GACGATCGCAGGACTCGCGCGCAACGAGCGCGCGTTCGTGCTGAGTTCGGG 3019  
QY 158 ValAspGluAla-----GluLeuValGlyPheSerAspSerLysLysArgLeu 173  
Db 3020 ATGGACGAGCTGTGTGTCACCGCCAGCTGTTGGTAGGATATTCGATGCAAAAGCTC 3079  
QY 174 LeuGluMetIleAspThrAsnAlaAsnAspGlyPro-----AlalysValIleCysValVal 192  
Db 3080 GTCCGGTGGCTG-----GCCGACGCGGAGCCGAAAGCTCAAGGTGCTTCATTTGT 3130  
QY 193 GlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGlu-----Glu 211  
Db 3131 GGATCCGAGGTGTGGCAACAGCACCTCGCCACAGAAATTCATGCTGTCATGCCCG 3190  
QY 212 AspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArg 231  
Db 3191 CGGTTGGATGCGCGCTTCGACTGCGCGGCTTCGTGCGAGCGCCCGGAGCCCTGACATG 3250  
QY 232 IleGluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeu 251  
Db 3251 ACGAAGATCTCCCGCATCTCTCACACTG-----CGGCCA 3289  
QY 252 LeuGlnGluLeuGlnGlyLysValValValGlnValHisHisLeuSerGluTyrLeuIle 271  
Db 3290 CAACATCAGCATCAGTCTTCGATGTTGGAGGTTGATCGACTCTCTGAAATATCCGG 3349  
QY 272 GluGluLeuLysGluLysArgTyrPheValValLeuAspAspLeuTrpIleLeuHisAsp 291  
Db 3350 ACGCATTTGCAAGATAAAGGTACTTCATCAATTAAGATTTATGGGCTTCATCAATG 3409  
QY 292 TrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
Db 3410 TGGGATATTGTTAGCCGT---GGTTTGCCTGATAATAAT---AGTTGCAGTAGAATACTA 3463  
QY 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
Db 3464 ATAACAACAAGAAATGAACCTGTAGCTTGGCATCTGTGATATATATCAGAGCAAT 3523  
QY 332 LeuAspPheLeuGlnMetAsnAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351

Db 3524 ATTAAGATTGATCCACTGGGTGATGATGCTCAAGTCAATTTGTTTTTCACTGAGTTGTT 3583  
Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
Db 3584 GGCAAGGAATGAATTTCTCTGACATCTTACTAGAGTTTCTCATGACATGATAAAAAA 3643  
Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnVal 391  
Db 3644 TGTGTGGCTTGCCTACTAGCATA---ACTATACAGCCAGACATTTTAAAGCCAGCTG 3700  
Qy 392 SerGluTrpGluLysPheTyrGluHisLeu-----ProSerGluLeuGlu 406  
Db 3701 TTAGATGGAATGAGCAATGGAATCACAATACAAAATCAATTCATCTTCCATTTTGAAG 3760  
Qy 407 IleAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsnHisLeuPro 426  
Db 3761 AAAATCTTACTTTGAGGGGATGAGGCAAGTACTCAACCTTATTACATATATCTTCCT 3820  
Qy 427 SerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLys 446  
Db 3821 CATTTGTTGAAAGCATGCTGTATACCTTAGCATCTACAAAGAGGACTACATAATTAGG 3880  
Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMet 466  
Db 3881 AAGGCCAATTTGTGAGGCAATGGATGGCTGAGGTTTCAATTCATCCATAGAAATAAA 3940  
Qy 467 ThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIleGln 486  
Db 3941 GTCATGGAAGAAGTTGAGGGAATTTATTTGATGAATTTGTTAGGGGCTTGTGTCAA 4000  
Qy 487 ArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleLeuArg 506  
Db 4001 CAGTAGATGTTAACTGCMAAATGAGGTATTTGATGTAGTACACCATGGTATTA 4060  
Qy 507 AspIleThrValSerIleSerArgGlnGluAsnPhe---ValLeuLeuProMetGlyAsp 525  
Db 4061 AATTTTCATCAGGTGAAGTCAATAGAGGAAATTTTCAAGATTCATTTGGATCATTCAG 4120  
Qy 526 GlySerAspLeuValGluGluAsnThrArgHisIleAlaPheHisGlySerMetSerCys 545  
Db 4121 ACAGTAGTAAGACATGTCAGCAAGTTCCGCGATCTCGCTTCACTTCAGCAATGCACAT 4180  
Qy 546 LysThr-----GlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly 561  
Db 4181 GATACACACCACTAGCAGGTTTGAGACTCTCAAGTTCGATCGATGGCATTTTGGGA 4240  
Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeu-----ArgMet 578  
Db 4241 -----CAGTCMAGTGTATGCTTCCATTCGAGATTATAGGCTT 4279  
Qy 579 LeuArgValLeu-----AspLeuGluAspValThrPheLeuIleThr 592  
Db 4280 TTTTCGAGTTCTGATTTCTTTGTTGTTGCTGATCAAGAGAAAAACAAGCTAT----- 4330  
Qy 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612  
Db 4331 -----GACCTCACAGCATTTTGAACGTGTATCAACTGAGATATCTGAAGATAACAGGT 4384  
Qy 613 SerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeu 632  
Db 4385 AATATCACAGTT---AAATCTCAGAGAGAATCCAGGACTACACACTTGCAGACACTG 4441  
Qy 633 AsnMetProSerThrTyrIleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeu 652  
Db 4442 GAAGCAGATGCAAGAGCAACTGCTGTCTTA---TTGATATTATTTCATCACAGTTGTTG 4498  
Qy 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672  
Db 4499 TTGCACCTTCGCTTGTGA----- 4516  
Qy 673 LysCysIleThrAsnThrIle-----CysLeuProLysValPheThrProLeuValSer 690  
Db 4517 -----CTACTTGATCTGCTCCCTCACTGTACAGGATACATCTTCACTC----- 4558

Qy 691 ArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSer 710  
Db 4558 ----- 4558  
Qy 711 GluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeu 730  
Db 4559 -----AGCATCCCAATGAGTGGAAAGCTCAACATCTCCGCATTTTA 4603  
Qy 731 GluTyrValAspIleArgArgThrSerSerArgAlaIleLysGluLeuGlnLeuSer 750  
Db 4604 AACATT-----GCAGTCATGCAAAATTTCCAG----- 4630  
Qy 751 LysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLeu 770  
Db 4630 ----- 4630  
Qy 771 TyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyIle 790  
Db 4630 ----- 4630  
Qy 791 SerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArg 810  
Db 4631 GATGACTTGACACTCTCAAGGACTGGGATCTCTCACTGCTCTTTCGCTGCTTGTGCA 4690  
Qy 811 ThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHis 830  
Db 4691 ACAGCGCCTGCGCAAGAATCGTC----- 4714  
Qy 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuIleLeu 850  
Db 4715 -----GCTGCCAATGAGGG-----TTC 4732  
Qy 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870  
Db 4733 GGGTCTCTCAAGTACTTCACTGTTGTC-----TGTCAGCACCATGC 4774  
Qy 871 LeuValPheLysThrGlyValAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
Db 4775 ATGACTTTTGGAGAGAGCAATGCCGAGTGTCAAGGTTA----- 4816  
Qy 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
Db 4817 -----AATCTAAGTTCAATGCCAACGAGTCAAG----- 4846  
Qy 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
Db 4847 -----CAGTATGACTCTAAGGACAGAGGTTGGAACACTTGTGCTCCCTTGCAGAG 4897  
Qy 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
Db 4898 ATCTCTGCAAGAAATTTGGGGCCTGATGATGATGAATCAACAACTGAAGTGGAGTCT 4957  
Qy 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963  
Db 4958 GCCTTGAGGATGCAATTCGCAAGCATCCGACGCCGAGCAGCTCTTATGTT-----GAT 5011  
Qy 964 ArgArgTyrHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGlnThrAla 983  
Db 5012 ATACAATGGGTGGATTGATCTTTTGTGCTGTAAGGAGAGAGACTTGGATGAAGATTGGCA 5071

## RESULT 6

US-09-360-186-2  
; Sequence 2, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staakawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1998-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 3099  
TYPE: DNA  
ORGANISM: Capsicum annuum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (93)..(2810)  
US-09-360-186-2

## Alignment Scores:

Pred. No.: 4,228-59 Length: 3099  
Score: 618.00 Matches: 253  
Percent Similarity: 40.8% Conservativity: 178  
Best Local Similarity: 24.0% Mismatches: 369  
Query Match: 11.7% Indels: 256  
DB: 3 Gaps: 41

US-10-656-394A-8 (1-1032) x US-09-360-186-2 (1-3099)

Qy 31 LeuLeuGluValGluLeuAspLeuTyrTrpTyrIleLysAspGluLeuLysThrMetGlnAla 50  
Db 51 TTGGTCATAGTCGCAAGGAC-----AAAACGAGAAATACAGTATATATGGCT 98  
Qy 51 PheLeuArgAlaAlaGluLeuMetLysLysLysAspGluLeuLysValTrpAlaGlu 70  
Db 99 CATGCAAGTGTGGCTTCTCTATGAGAACATAGATCTCTCTG---ACATTCATTCG 155  
Qy 71 GlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPheLysValHisLe 90  
Db 156 CCGATGCAATCTATCTCTGTGATCAGAGAAAGACTTTGCGCTCTTCGTGAAAAAGTT 215  
Qy 91 GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIleAlaLe 110  
Db 216 AGTTCCTCGAGATATT-----GTCAAGAACTTGAGAAACAAATGTTTGGG 266  
Qy 111 ArgIleHisLeuLysSerArgValGluGluValSerSer----- 124  
Db 267 GAAATGACGGAATTTTGAAGTAGAGTAAGAGAGTTGCAAGTGTGCTGAATACAAATT 326  
Qy 124 ----- 124  
Db 327 CAAGTACTAACAGGAAGTCTACTGGGAGAAATAAAGCCAGAAAGGAGGCGT 386  
Qy 125 ArgAsnThrArgTyrSerLeu----- 131  
Db 387 CGAAGGTTTCGTCAAGGCTGCAACAGTAGCAGGACATGGATCATATCTCGAAAGAG 446  
Qy 132 ---ValIysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGluAspIle 150  
Db 447 TCAGCAAAAGATCCAGATTAAGAAACAAAGTATCAAGGAAATCATTTGGTTTCATGATTT 506  
Qy 151 ArgAsnGlnSerAlaArgAsnValAspGluAlaGlu-----LeuValGlyPheSerAsp 168  
Db 507 ---TCAAGTTCACAAACCAATATTTTGAAGGTTAAGAACATATATGTTGACGCTGATGAT 563  
Qy 169 SerLysArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysVal 188  
Db 564 CAAAGGAACAGTGTGTAGAGATCTG---ACTAGAGCTACTCTGGGAAACCAAGTTC 620  
Qy 189 IleCysValValGlyMetGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGlu 208  
Db 621 ATCCGATGTCGGATGGGAGGATAGTAAACCAACCTTAGCAAAAGAAAGTTTAC--- 677  
Qy 209 SerGluGluAspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSer 228  
Db 678 AATGATGAATCAATCTATGCGGTTTGAATGTTCAATGCTGGGCTACCATCTCAACAG 737  
Qy 229 PheHisArgIleGluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeu 248  
Db 738 CACACAAAAAGGAATTTTGTGGGCTTCTGCAATTCACAAATCAAAATGGATGACAGG 797

Qy 249 AspGlnLeuLeuGlnGluLeuGlnGlyLysValValGlnValHisLeuSerGlu 268  
Db 798 GTTAAGATGATTGTGAAGCAGAG-----CTACAGAC 830  
Qy 269 TyrLeuIleGluGluLeuLysGluLysArgTyrPheValValLeuAspLeuTrpIle 288  
Db 831 ATGTTTACAGAAAAGTTTAAAGAGAAAGAGTACTTAATTTGTTCTTGGATCATCTGGAGT 890  
Qy 289 LeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysGlySer 308  
Db 891 TGTGAAGTGTGGATGGCGTGAGACGA---TGTCTTCCCACTGAAGCAATCCAGGAGT 947  
Qy 309 ArgIleValIleThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeu 328  
Db 948 CGAATACTGTTGACTACCCGTAAATGATGATAGTACTTGTATGCTGGTGTAGAGAATTT 1007  
Qy 329 ValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThr 348  
Db 1008 TCTTTGCGGATGAGCTTTCATGGATCAAGATGAGAGTTGGAGT---CTTTTCAAAAGTGA 1064  
Qy 349 AsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIle 368  
Db 1065 GCATTTTCAAGTGAAGCATTACCA-----TATGAGTTCGAGACTGTTCGAAAGCAATC 1118  
Qy 369 ValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleClyAlaValLeuAlaThr 388  
Db 1119 GCAGATGAATGTCACGGGTTACCACTAATCTATTTGTCGTGGTTCAGGGCTTCTCAATCT 1178  
Qy 389 LysGln---ValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIle 407  
Db 1179 AAAGGCAATAGAGATTCGAAACCTGTTGCTAAAGATGTCAAGTCAATTCGTCAAAAT 1238  
Qy 408 AsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsnHisLeuProSer 427  
Db 1239 GATCTCGAT---GAACGATGTTCACTGCTGCTGGGTGAGTTACCATCACTGCAAGC 1295  
Qy 428 HisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArg 447  
Db 1296 GATCTAAAACATGCTCTTCGATTCGGAATTTTCCAGAGACAGATGATATCCAGTG 1355  
Qy 448 AsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThr 467  
Db 1356 AAGAAATTTGATGAGATCATGATGCTGAGGGTCTCTG---AAGTTGGAATGAT 1409  
Qy 468 ThrLysAspValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIle----- 485  
Db 1410 TTGGAGAGAGAGGTTGAGAGTGTTCAGAGAGCTTTCAGATAGATGTCTAGTCTCTGTC 1469  
Qy 486 ---GlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIle 504  
Db 1470 AGCAAGAGAAAGTCGAGATGGAACA-----AAAATAGATCATGTAAGGTTTCATGATCTA 1523  
Qy 505 IleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGly 524  
Db 1524 ATATATGACCTGCTGCTGAGAGAGTTCAAAGGGAGAACATTTTATCATG----- 1574  
Qy 525 AspGlySerAspLeuVal----- 530  
Db 1575 ---AACGACATGTTCTTTGACGTATCATATCCAGAAATGTTTCATATCTCTGTATGTAT 1628  
Qy 531 ---GlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThrGlyLeu 549  
Db 1629 AAAATGACGCGCTTAAAGCGCGTGATGAGTGAATAATTAATTTATTTGTCCTATGCTCT 1688  
Qy 550 AspTrpSerIleIle----- 554  
Db 1689 TATAGGCTCTTCTTACCCCTGTAAATCGTCAGTTGAGAGATCATGCAACCAACATCTT 1748  
Qy 555 ---ArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCys 572  
Db 1749 TTGAACGAAACCAATCTGTTTCTCTTTTCATCTTGGCGCTTTATATTATGTTCTCAAA 1808  
Qy 573 ProAsp-----GlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeu 590

Db 1809 TCAGAGTTGTTTCATTTCAAAATTAAGTCTTGGAGCTGAGA----- 1853  
Qy 591 IleThrGlnLysAspPheAsp-----ArgIleAlaLeuLeuCysHisLeuLys 606  
Db 1854 -----CACAGACAGATTGATGGTTTCCTCGAGAGATACCTAAGCCCTCATCTGGTTGAGG 1907  
Qy 607 TyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuProArgSerIleGlyLysLeu 626  
Db 1908 TACCTATCATTTG-----TTGAGTATGGGAATTTGATGATACCTCCAGAAATTTGCAAGTTA 1964  
Qy 627 GlnGlyLeuGlnThrLeuAsnMetPro-----SerThrTyrIleAlaLeuProSer 644  
Db 1965 TCGAATCTGCAGACATCATTTGTCACGGTTTCGATCAGATATATAATTTTTCCTGAG 2024  
Qy 645 GluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAsp 664  
Db 2025 GAAATTTGGAACTAATAAGCAATTAAGGCATCTTAA----- 2060  
Qy 665 AsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysVal 684  
Db 2061 -----CTGCCAGATT 2072  
Qy 685 PheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaLeuHisMetAla 704  
Db 2073 TATTTGCCA----- 2081  
Qy 705 ThrLysSerCysTyrPheSerGluSerIleGlyValLysValProLysGlyIleGly---Lys 723  
Db 2082 -----GATTTGCCAGTGGATCT-----GTTGACAAAGAGGAGGACTTGGAT 2123  
Qy 724 LeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSerArgAlaIle 743  
Db 2124 TTTTCAAACTTCAAACTATTCTTCTGTCTCCAGTTTGTCCACGAGGAGGATTAT 2183  
Qy 744 LysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThr 763  
Db 2184 -----ATGGGG---ATTGAGATGTCMAAATAGGAATCAGTGAATTAAGAT--- 2231  
Qy 764 LysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeu 783  
Db 2231 ----- 2231  
Qy 784 HisValAspAlaAlaGlyIleSerAspGlyGly----- 794  
Db 2232 -----GACTATAAAGTTTTCGGGACTCTGGGCTCCCAACATCTTCTATCTGCAG 2285  
Qy 795 ThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeu 814  
Db 2286 CAACCTTGAATATTGAGTCTTATATCTGTTGATTATAGCCTTTTGGCCAGTGATCATTTCA 2345  
Qy 815 AspGlyIleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHisLeuLysIle 834  
Db 2346 AGTGCA-----AAAGCTTTTCCAGCAACGCTCAAGAGTTG---NAGTTGGAAGAACT 2396  
Qy 835 TyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuPro 854  
Db 2397 TATCTAAGCTGTCTACTACTTGGAC-----ATCATAGCTGAGTTGCCT 2438  
Qy 855 AsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys----- 870  
Db 2439 AACCTTGAGTGCTGAAGCTCATGGATGACGCTTGTGTGGTGAAGATGGCATCAATT 2498  
Qy 871 -----LeuValPheLys----- 874  
Db 2499 GTTATGGGATTTAATFCGATTGAAGCTTTTGTCTAATAATATAATATTTTCTCAAGTTCTGG 2558  
Qy 875 -----ThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGln 891  
Db 2559 AAAGCCCAATATGACAAATTTTCTGCTCTGAGGCTCATGATTAGAGTTGCCAAAT 2618  
Qy 892 LeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGlyIle 911

Db 2619 TTGAAGAGATACCCATTTGAGTTGGAGATATACACACTACAGCTGATTGAGTTAAGA 2678  
Qy 912 GluCysArgLeuGluSerGlyIleThrGlyIleHisLeuProLysLeuLysGluIle 931  
Db 2679 GAGTGTCTCT-----CCCAAACTTGGGAATCT 2705  
Qy 932 ProIleArgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyValAlaAla 951  
Db 2706 GCTGCACGAATTTCAAGAAACAAGAACCTCGGA-----AACAAACCTGTGATGTT 2759  
Qy 952 HisProAsnArgProValLeuLeuMetTyrSerAspArgTyrHis 967  
Db 2760 CGTATCTCAATCTTGAAGAGAGTGTCTGATTGAGAAGACAT 2807

## RESULT 7

US-09-864-680A-2  
; Sequence 2, Application US/09864680A  
; Patent No. 6762285  
; GENERAL INFORMATION:  
; APPLICANT: Staekawicz, Brian J  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Tai, Thomas H  
; TITLE OF INVENTION: B52 RESISTANCE GENE  
; FILE REFERENCE: 42250/234021 (5830-4A)  
; CURRENT APPLICATION NUMBER: US/09/864,680A  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 09/360,186  
; PRIOR FILING DATE: 1999-07-23  
; PRIOR APPLICATION NUMBER: US 60/093,957  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Capsicum annum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (93)..(2810)  
; OTHER INFORMATION:  
US-09-864-680A-2

## Alignment Scores:

Pred. No.:	4,22e-59	Length:	3099
Score:	618.00	Matches:	253
Percent Similarity:	40.8%	Conservative:	178
Best Local Similarity:	24.0%	Mismatches:	369
Query Match:	11.7%	Indels:	256
DB:	3	Gaps:	41

US-10-656-394A-8 (1-1032) x US-09-864-680A-2 (1-3099)

Qy 31 LeuLeuGlyValGluLysAspIleTyrIleLysAspGluLeuLysThrMetGlnAla 50  
Db 51 TTGCTCATAGTCGCAAGGAC-----AAAAACGAGATACAGTATATATGCT 98  
Qy 51 PheLeuArgAlaAlaGluLeuMetLysLysAspGluLeuLysValTrpAlaGlu 70  
Db 99 CATCAAGTGTGGCTCTCTTATGAGAACAAATAGAAATCTCTTG---ACATTCAATTG 155  
Qy 71 GlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPheLysValHisIle 90  
Db 156 CCGATGCAATCTCTATCTCTGATCAGAGAAAGAAATTTGGCTCTTCGTGAAAAAGTT 215  
Qy 91 GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIleAlaIle 110  
Db 216 AGTTCCCTCGAAGTATT-----GTCAGAACTTTGAGAAAAACAATGTTTTTGGG 266  
Qy 111 ArgIleHisLeuLysSerArgValGluGluValSerSer----- 124  
Db 267 GAAATGCGGATTTTGAAGTAGAGGTGAAGAGTTGCAAGTGTGCTGTAATACAAATT 326  
Qy 124 ----- 124

Db 327 CAACTGAGACTAACAGGAACCTGTACTGGGAGAAAATAAAGCCAGAAAAAAGGCGGT 386  
Qy 125 AtgAsnThrArgTyrSerLeu-----  
Db 387 CGAAGGTTTCGTCAAAGCTGCAACAGTAGCAGAGGACATCATATCTCGAAGAG 446  
Qy 132 ---ValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGluAspIle 150  
Db 447 TCACAAAGATCCAGATAAAGGAAACAAAGTATCAAAAGGAATCATTTGGTTTCATGATTT 506  
Qy 151 ArgAsnGlnSerAlaArgAsnValAspGluAlaGlu-----LeuValGlyPheSerAsp 168  
Db 507 ---TCAGTTCAACAAACGATATTTGAAGTTAAGAACATATATGTTGGAGCTGATGAT 563  
Qy 169 SerLysGlyArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysVal 188  
Db 564 CAAAGGAAACAGTTGTTAGAAGATCTG---ACTAGAAGCTACTCTGGGGAACCCAAAGTC 620  
Qy 189 IleCysValValGlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGlu 208  
Db 621 ATCCGATTTGGGATGGAGGCGATAGTAAACACCTTAGCAAAAGAGTTTAC--- 577  
Qy 209 SerGluGluAspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSer 228  
Db 678 AATGATGAATCAATTCATCGCGTTTGTATGTCATGCTGGGCTACCATATCTCAACAG 737  
Qy 229 PheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeu 248  
Db 738 CACAAACAAAGAAATTTTGTGGGCTTCTGCAATTCACATCAAAATGGATGACAG 797  
Qy 249 AspGlnLeuGlnLeuGlnGlyLysValValGlnValGlnValHisLeuSerGlu 268  
Db 798 GTTAAGATGATTGGTGAACACAG-----CTAGCAGAC 830  
Qy 269 TyrLeuIleGluLeuLysGlyLysArgTyrPheValValLeuAspLeuTrpIle 288  
Db 831 ATGTTACAGAAAAGTTTAAAGAGAGAGAGTACTTAATGTCTGGATGATATCTGGAGT 890  
Qy 289 LeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnLeuLysGlySer 308  
Db 891 TGTGAAGTGTGGGATGGCGTGAGACGA--TGCTTTCCAACTGAAGACATGACAGGAGT 947  
Qy 309 ArgIleValIleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeu 328  
Db 948 CGAATATGTTGACTACCGCTAATGATGAAGTAGCTTGTATGCTGGTGTAGAGAATTT 1007  
Qy 329 ValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThr 348  
Db 1008 TCITTCGGATGAGCTTCATGATCAAGATGAGAGTTGGAGT---CTTTTCAAAAGTGCA 1064  
Qy 349 AsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIle 368  
Db 1065 GCATTTTCAAGTGAAGCATTACCA-----TATGAGTTTCGAGACTGTTGAAAGCAATC 1118  
Qy 369 ValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThr 388  
Db 1119 GCAGATGAATGTACCGGTTTACCACTACTATGTCGGTGGTGGAGGCTTCTCAATCT 1178  
Qy 389 LysGln---ValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIle 407  
Db 1179 AAAGGACATAGAGATTGGAAAACGTGTTCTAAGATGTCAAGTCAATTCGTGCACAAAT 1238  
Qy 408 AsnProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSer 427  
Db 1239 GATCCTGAT---GAACGATGTTCAAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1295  
Qy 428 HisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArg 447  
Db 1296 GATCTAAAACATGTCTTCTGCAATTTTCCAGAAAGACAGTATATCCAGTG 1355  
Qy 448 AsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThr 467

Db 1356 AAGAAATTTGATGATCATGATCGATCGGCTGAGGGGTTCTCTG-----AAGTTGGAATGAT 1409  
Qy 468 ThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuLeuAsnArgSerMetIle----- 485  
Db 1410 TTGGAAGGAGAGGTTGAGAAAGTGTTCGAAGAGCTTGTGATAGATGTCTAGTCTCGTC 1469  
Qy 486 ---GlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIle 504  
Db 1470 ACCAAGAGAGTTCAGATGGNACA-----AAATTAGATCATGTAAGTTCATGATCTA 1523  
Qy 505 IleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGly 524  
Db 1524 ATATATGACCTGTGCTGAGAGAGTTCAAAGGAGAGAACATTTTATCATG----- 1574  
Qy 525 AspGlySerAspLeuVal----- 530  
Db 1575 -----AACGACATGTTCTTGAGCTATCATATCCAGATGTTTCATATCTCTGATGAT 1628  
Qy 531 ---GlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThrGlyLeu 549  
Db 1629 AAAATGCAAGCCCTTTAAGCGGTGACTGGTGTGATGAAATTAATTAATTGTCCTATGCTCT 1688  
Qy 550 AspTrpSerIleIle----- 554  
Db 1689 TATAGGCTCTTCTTACCCCTGTAAATCGTCAGTTGAGAGATCATGACAAACAATCTT 1748  
Qy 555 -----ArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCys 572  
Db 1749 TTGAAACGAACCCATCTCTCTTTCTCTTTTCTGAGCCTTATATATTTATCTCTCAAA 1808  
Qy 573 ProAsp-----GlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeu 590  
Db 1809 TCAGAGGTTGTTCTATTCAAATTAATCTCAAAAGTCTTGAGCTGAGA----- 1853  
Qy 591 IleThrGlnLysAspPheAsp-----ArgIleAlaLeuLeuCysHisLeuLys 606  
Db 1854 -----CACAGACAGATTGATGTTTCCCTCGAGAGATACATAAGCCCTCATCTGTTGAG 1907  
Qy 607 TyrLeuSerIleGlyTyrSerSerIleTyrSerLeuProArgSerIleGlyLysLeu 626  
Db 1908 TACCTATCATTTG---TTCAGCTATGGAAATTTGATGATCTCCAGAAATTTGCAGGTTA 1964  
Qy 627 GlnGlyLeuGlnThrLeuAsnMetPro-----SerThrTyrIleAlaAlaLeuProSer 644  
Db 1965 TGGAACTCTGCAGACATTCATTTTCAAGGTTTCGATCAGATATATAATTTTGTCTGAG 2024  
Qy 645 GluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAsp 664  
Db 2025 GAAATTTGGGAACATAATCAATTAAGGATCTTAA----- 2060  
Qy 665 AsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysVal 684  
Db 2061 -----CTGCCACGATTT 2072  
Qy 685 PheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAla 704  
Db 2073 TATTTGCCA----- 2081  
Qy 705 ThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGlyIleGly---Lys 723  
Db 2082 -----GATTGCCCAAGTGGATCT-----GTTCAAGAGGAGGACTTGGAT 2123  
Qy 724 LeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSerArgAlaIle 743  
Db 2124 TTTTCAAACTTACAACTATTTCTTACTTGTCTCCAGTTGTTGTCAGAGGAGGTTATT 2183  
Qy 744 LysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThr 763  
Db 2184 -----ATGGGG---ATTCAAGATGTCAAAATTAGAATCATGTCAGGAAATAGGAT--- 2231  
Qy 764 LysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeu 783  
Db 2231 ----- 2231

Alignment Scores:	
Pred. No.:	7,968-57
Score:	614.00
Percent Similarity:	40.4%
Best Local Similarity:	24.0%
Query Match:	11.7%
DB:	3
Length:	31491
Matches:	250
Conservative:	174
Mismatches:	355
Indels:	264
Gaps:	41





; APPLICANT: Staskawicz, Brian J  
 ; APPLICANT: Dahlbeck, Douglas  
 ; APPLICANT: Tai, Thomas H  
 ; TITLE OF INVENTION: B62 RESISTANCE GENE  
 ; FILE REFERENCE: 42250/234021 (5830-4A)  
 ; CURRENT APPLICATION NUMBER: US/09/864,680A  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/360,186  
 ; PRIOR FILING DATE: 1999-07-23  
 ; PRIOR APPLICATION NUMBER: US 60/093,957  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 31491  
 ; TYPE: DNA  
 ; ORGANISM: Capsicum annuum  
 ; US-09-864-680A-1

Alignment Scores: Pred. No.: 7,96e-57 Length: 31491  
 Score: 614.00 Matches: 250  
 Percent Similarity: 40.7% Conservative: 174  
 Best Local Similarity: 24.0% Mismatches: 355  
 Query Match: 11.7% Indels: 264  
 DB: 3 Gaps: 41

US-10-656-394A-8 (1-1032) x US-09-864-680A-1 (1-31491)

Qy 34 valGluLysAspIleTrpTyrIleLysAspGluLeuLysThrMetGlnAlaPheLeuArg 53  
 Db 1447 GTCCGAAGGAC-----AAAAACGAGAAATCAGTATATATGGCTCATGCAAGT 1494  
 Qy 54 AlaAlaGluLeuMetLysLysAspGluLeuLysValTrpAlaGluGlnIleArg 73  
 Db 1495 GTGGCTCTCTTATGAGAACATAGATCTCTCTG--ACATTCAATTCGCGCATGCAA 1551  
 Qy 74 AspLeuSerTyrAspIleGluAspSerLeuAspGluPheLysValHisIleGluSerGln 93  
 Db 1552 TCTATCTCTGTGATCAGACGAAAGATTTGGCCTCTTCGTGAAAAGTTAGTTCCTCG 1611  
 Qy 94 ThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIleAlaIleArgIleHis 113  
 Db 1612 GAAGTATTT-----GTCAAGAACTTTGAGAAACAAATGTTTGGGGAATGACG 1662  
 Qy 114 AsnLeuLysSerArgValGluGluValSerSer----- 124  
 Db 1663 GATTTTGAAGTAGAGGTAAAGAGGTTGCAAGTCTGCTGCTGAATACAAATTCAACTGAGA 1722  
 Qy 125 ----- 127  
 Db 1723 CTAAACAGGAACGTACTGGGAGAAATAAAGCCAGAAAGGCGGTGCAAGTTT 1782  
 Qy 128 ArgTyrSerLeu-----ValLys 133  
 Db 1783 CGTCAAGGCTGCAACAAAGTAGCAGAGGACATGGATCATATCTCGAAAGAGTCGCAAG 1842  
 Qy 134 ProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGluAspIleArgAsnGln 153  
 Db 1843 ATCCAAGATAAGGAAACAAAGATATCAAGGAATCATTTGTTTCATGATTTT---TCAAGT 1899  
 Qy 154 SerAlaArgAsnValAspGluAlaGlu-----LeuValGlyPheSerAspSerLysLys 171  
 Db 1900 TCAACAAACGATATTTTGAAGGTTAAGAACAAATATGTTGGACGCTGATGATCAAGAGAA 1959  
 Qy 172 ArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysValIleCysVal 191  
 Db 1960 CAGTTGTTAAGACATCTG---ACTAGAGCTACTCTGGGAACCCAAAGTATCCCGATT 2016  
 Qy 192 ValGlyMetGlyGluGlyThrAlaLeuSerArgLysIlePheGluSerGluGlu 211  
 Db 2017 GTCGGATGGGAGGATAGGTAAACCAACCTTAGCAAAAGAGTTTAC---AATGATGAA 2073

Qy 212 AspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArg 231  
 Db 2074 TCAATTTCTATGCCGTTTGTATGCTGCTGGGGTACCATATCTCAACAGCACACAAA 2133  
 Qy 232 IleGluLeuLysAspMetIleArgGlnLeuGlyProSerSerLeuAspGlnLeu 251  
 Db 2134 AAGGAAATTTGCTGGGCTTCTGCATTCACAAATCAAAATGATGATCAGGGGTTAAGTG 2193  
 Qy 252 LeuGlnGluLeuGlnGlyLysValValGlnValHisIleSerGluTyrLeu 271  
 Db 2194 ATTGGTGAAGCAGAG-----CTAGCAGACATGTTTACAG 2226  
 Qy 272 GluGluLeuLysGluLysArgTyrPheValValIleAspAspLeuTrpIleLeuHisAsp 291  
 Db 2227 AAAAGTTTAAAGAGAAAGAGGTACTTAATTTGTTCTGGATGATATCTGGAGTTGTGAGTG 2286  
 Qy 292 TrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
 Db 2287 TGGGATGGCTCAGACGA--TGCTTTTCCAACTCAAGACAAATCGAGGAGTCCAAATCTG 2343  
 Qy 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
 Db 2344 TTGACTACCCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2403  
 Qy 332 LeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351  
 Db 2404 ATGAGCTTTCATGGATCAAGATGAGATGAGTTGGAGT---CTTTTCAAAAGTCAGCATTTTCA 2460  
 Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
 Db 2461 AGTGAAGCATACCA-----TATGATTCGAGACTGTTGGAAAGCAATCCAGATGAA 2514  
 Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGln--- 390  
 Db 2515 TGTACCGGTTTACCACATACTATTGTCGTGGTTCAGGGCTCTCAAAATCTAAAGGACA 2574  
 Qy 391 ValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsnProSer 410  
 Db 2575 ATAGAAGATTGGAAACTGTTGCTAAAGATGTCAAGTCATCTGTCACAAATGATCCTGAT 2634  
 Qy 411 LeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLys 430  
 Db 2635 --GAACGATGCTCACGCTGCTGGGTTGAGTTACGATCCTTGCACAGCGCATCTAAA 2691  
 Qy 431 ProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeu 450  
 Db 2692 ACATGCTCTCTGCAATTTCCGAAATTTTCCAGAGACAGTGATATTCAGATGAAGAAATTG 2751  
 Qy 451 ValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAsp 470  
 Db 2752 ATGAGATCATGATGCTGAGGGGTTCTCTG-----AAGTTGGAATAATGATTTGGAAGA 2805  
 Qy 471 ValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIle-----GlnArg 487  
 Db 2806 GAGGTTGAGAAGTGTTCGAAAGAGCTGTGATAGATGCTAGTCTCTGCTCGTCAGCAAGA 2865  
 Qy 488 SerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAsp 507  
 Db 2866 AGTCGAGATGGAACA-----AAATATGATCATGTAAAGTTTCATGATCTAATATGAC 2919  
 Qy 508 IleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySer 527  
 Db 2920 CTGTGCTGAGAGAGTTCAAAGGGAGAACATTTTATCATG-----AAC 2964  
 Qy 528 AspLeuVal-----GlnGlu 532  
 Db 2965 GACATTTGTTCTGACGATCATATCCAGATGTTTCATCTCTGATGATATAAATGACG 3024  
 Qy 533 AsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThrGlyLeuAspTrpSer 552  
 Db 3025 CCCTTTAAGCGCGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3084  
 Qy 553 IleIle-----Arg 555

Db 3085 CTTCTTACCCCTGTAAATCGTCAGTTGAGAGATCATGACACAAACAATCTTTTGAACGA 3144  
Qy 556 SerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAsp--- 574  
Db 3145 ACCATTCTGTTTCTCTTTTCATCTTGAGCCTTTATATTATGTTCTCAATCAGAGTT 3204  
Qy 575 ---GlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGln 593  
Db 3205 GTTCATTTTCAATTAATCAAGTCTTGAGCTGAGA-----CAC 3243  
Qy 594 LysAspPheAsp-----ArgIleAlaLeuLeuCysHisLeuLysTyrLeuSer 609  
Db 3244 AGCAGATTGATGTTTCCCTCGAGAGATCACTAAGCCTCATCTGTTGAGGTACCTATCA 3303  
Qy 610 IleGlyTyrSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeu 629  
Db 3304 TTG---TTCAGCTATGGGAATTTTCGATGTACCTCCAGAAATTTGCAGGTTATGGAATCTG 3360  
Qy 630 GlnThrLeuAsnMetPro-----SerThrTyrIleAlaAlaLeuProSerGluIleSer 647  
Db 3361 CAGACATTCATTGTTCAACGGTTTCGATCAGATATATAATTTTCTGAGGAATTTGG 3420  
Qy 648 LysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSer 667  
Db 3421 GAACATTAATGCAATTAAGCATCTTAAA----- 3447  
Qy 668 LeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysValPheThrPro 687  
Db 3448 -----CTGCCAGATTTTATTGCGCA 3468  
Qy 688 LeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSer 707  
Db 3469 -----GAT 3471  
Qy 708 CysTrpSerLysIleGlyValLysValProLysGlyIleGly---LysLeuArgAsp 726  
Db 3472 TGCCCAAGTGGATCT-----GTTGACAAAGAGAGGCACTTGGATTTTCAAC 3519  
Qy 727 LeuGlnValLeuGluTyrValAspIleArgThrSerSerArgAlaIleLysGluLeu 746  
Db 3520 TTACAACATTTCTTACTTGTCTCCAGTTGTCACGAGGAGGTTAT-----ATG 3573  
Qy 747 GlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrGlySerThrLysGluLys 766  
Db 3574 GGG---ATTGAGAAATGTCAAAATAGGAATCAGTGAATTAAGAT----- 3618  
Qy 767 CysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAsp 786  
Db 3619 -----GAC 3621  
Qy 787 AlaAlaGlyIleSerAspGlyGly-----ThrLeuGlu 797  
Db 3622 TATAAAGATTTTCGGGACTCTGGGCTTCCCAACAATCTTGTCTATCTGCGACCACTTGA 3681  
Qy 798 CysLeuAspSerIleSerProProLeuLeuArgThrLeuValLeuAspGlyIle 817  
Db 3682 ATATTGAGCTTATATCTGTTGATTATAGCTTTTGGCAGTGATATTTCAAGTGCA--- 3738  
Qy 818 LeuGluGluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeu 837  
Db 3739 ---AAAGCTTTTCCAGCAACGCTCAAGAAAGTTG---AAGTTGGAAGAACTTATCTAAGC 3792  
Qy 838 ArgSerLysLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMet 857  
Db 3793 TGTCTATCTTGGAC-----ATCATAGCTGAGTTGCTCAACCTTGG 3834  
Qy 858 ValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys----- 870  
Db 3835 GTCTTGAAGCTGATGATGACGCTTGTGTTGGTGAAGAAATGGCATCCATTTGTTATGGGA 3894  
Qy 871 -----LeuValPheLys----- 874

Db 3895 TTTAATCGATTGAAGCTTTTGTCTAATTAATATAGTTTTTCTCAAGTTCTGGAAGCCACA 3954  
Qy 875 ThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGlu 894  
Db 3955 AATGCAATTTTCTGCTTGTGAGCGCCTCATGATTAGAGTTGCAAAATTTGAAGAG 4014  
Qy 895 IleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIleGlyGluCysArg 914  
Db 4015 ATACCATTTGATTTGCAGATATACACACTACACTGATTGAGTTAAGAGAGTGTCT 4074  
Qy 915 LeuGluSerGlyIleThrGlyIleLeuHisLeuProLysLeuLysGluIleProLeuArg 934  
Db 4075 -----CCCAAACTTGGGGAATCTCTGCAACA 4101  
Qy 935 TyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsn 954  
Db 4102 ATTCAAGAAAGAACAGAGAGCTTCGA-----AAC 4131  
Qy 955 ArgProVal 957  
Db 4132 AACCCCTGTG 4140

RESULT 10  
US-09-360-186-4  
; Sequence 4, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2718  
; TYPE: DNA  
; ORGANISM: Capsicum annum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2718)  
US-09-360-186-4

Alignment Scores:  
Pred. No.: 3,1e-58 Length: 2718  
Score: 609.50 Matches: 243  
Percent Similarity: 42.7% Conservative: 188  
Best Local Similarity: 24.1% Mismatches: 361  
Query Match: 11.6% Indels: 219  
DB: 3 Gaps: 40

US-10-656-394A-8 (1-1032) x US-09-360-186-4 (1-2718)

Qy 42 LysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaGluLeuMetLysLysLys 61  
Db 91 AGAGAAGAACTTTCGCTCTTCGTGAAAAAAGTTAGTTCCCTGGAAGTATTTGTCAAGAAC 150  
Qy 62 AspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAsp 81  
Db 151 TTTGAGAAAACAATGTTTTTGGGAA---ATACCGATTTTCAAGTAGAGTAAAGAA 207  
Qy 82 -----SerLeuAspGluPheLysValHisIle-GluSerGlnThrLeuPheArgGlnLeu 99  
Db 208 GTTGAAGTGTGCTGTAATCAAACTGAGACTAACAGAACTGTCTGCGGAA 267  
Qy 99 uValLysLeuArgGluArgHisArgIleAla-----IleArgIleHisAsnLeuLysSe 117  
Db 268 ATAAAGCCAGAAAAAAGCGCGTGGAGGTTTCGTCAAGCTTCGCAAGTAGCA 327  
Qy 117 rArgValGluGluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSe 137

Db 328 GAGGACATGATCATATCTGGAAAGAGCTGCAAAAGATCCAGAT-AAA----- 375  
Qy 137 rGlyThrGluLeuLeuAspMetAspSerTyrAlaGluAspLeuAlaArgAs 157  
Db 376 -GGAAACAAGATCAAGGAATCATGTTGTTTCATGATTTT---TCAAGTTCAACAACGA 431  
Qy 157 nValAspGluAlaGlu-----LeuValGlyPheSerAspSerLeuValArgLeuLeu 175  
Db 432 TATTTTGAAGGTTAAGAACATATGTTGGAGCTGATGATCAAGGAACAGTTGTTAGA 491  
Qy 175 uMetIleAspThrAsnAlaAsnAspGlyProAlaIleValIleCysValValGlyMetG1 195  
Db 492 AGATCTG---ACTAGAAGCTACTCTGGGGAACCCAAAGTCTCCGATTTGGGATGG 548  
Qy 195 yGlyLeuGlyValThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLys 215  
Db 549 AGCATAGTAAACAAACCTTTAGCAAAAGAGTTTAC---AATGATGAATCAATTCATG 605  
Qy 215 sAsnPheProCysAsnAlaIleThrValSerGlnSerPheHisArgIleGluLeu 235  
Db 606 CCCTTTTGATGTTTCATGCTGGCTACCATATCTCAACAGCACACAAAAAGGAATTTT 665  
Qy 235 uLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGluLe 255  
Db 666 GCTGGGCTTCTGCAATCCCAATCAAAATGGATGACAGGTTAAGATGATGGTGAAGC 725  
Qy 255 uGlnGlyLysValValGlnValHisHisLeuSerGluTyrLeuIleGluLeuLeu 275  
Db 726 AGAG-----CTAGCAGACATGTTACAGAAAGTTTAA 758  
Qy 275 sGluLysArgTyrPheValValLeuAspLeuTrpIleLeuHisAspTrpAsnTrpI1 295  
Db 759 GAGAAAGAGGTACTTAATGTTCTGGATGATATCGAGTTGTCAAGTGTGGGATGGCGT 818  
Qy 295 eAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleValIleThrAr 315  
Db 819 GAGACCA---TGCTTTCCAACTGAAGACAATGACGAGGAGTGAATCTGTTGACTACCG 875  
Qy 315 sAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPhe 335  
Db 876 TAATGATGAAGTAGCTGTTATGCTGTGTAGAGAAATTTTCTTCGGATGAGCTTCAT 935  
Qy 335 uGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAsp 355  
Db 936 GGATCAAGATGAGAGTTGGAGT---CTTTCAAAAGTGCAGCATTTTCAAGTGAACAT 992  
Qy 355 tGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArg 375  
Db 993 ACCA-----TATGAGTTTCGAGACTGTTGGAAAGCAAAATGCGAGATGAATGTCACGGGTT 1046  
Qy 375 uProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGln---ValSerGluTr 394  
Db 1047 ACCACTAATATGTTGCTGTTGCGGCTTCTCAATCTTAAAGGACATAGAGATG 1106  
Qy 394 pGluLysPheTyrGluHisLeuProSerGluLeuGluLeuAsnProSerLeuGluAla 414  
Db 1107 GAAACCTGTTGTAAGATGCAAGTCAATTCGTACAAATGATCCTGAT---GAACGATG 1163  
Qy 414 uArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPhe 434  
Db 1164 TTCACGTGCTGCTGGTTGAGTTAGATCACTTGCACAGCGATCTTAAACATGCTTCT 1223  
Qy 434 uTyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTr 454  
Db 1224 GCATTTTCGGAATTTTTCAGAGACAGTATATTCAGATGATGATGATGATGATGATG 1283  
Qy 454 pIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyLys 474  
Db 1284 GATGGCTGAGGGTTCTCTG-----AGTTGGAATGATTTGAGAGAGAGGTTGAGAA 1337  
Qy 474 rTyrPheAsnGluLeuLeuAsnArgSerMetIle-----GlnArgSerArgValG1 491  
Db 1338 GTGTTTGAAGAGCTTGTGATGATGTTCTAGTCTCGTCAGCAAGAGAGTGCAGATGG 1397

Qy 491 yIleAlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValse 511  
Db 1398 AACA-----AAAATTAGATCATGTAAGTTCATGATTAATATATGATGACCTGTGGTGAG 1451  
Qy 511 rIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuVal-- 530  
Db 1452 AGAAGTTCAAGAGGAGAACATTTTATCATG-----AACGACATTTGTTCT 1496  
Qy 531 -----GlnGluAsnThrArgH1 536  
Db 1497 TCACGTATCATATCCAGAAATGTTTCATATCTCTGTATGTATATAAAATGACGCCCTTAAAGCG 1556  
Qy 536 sIleAlaPheHisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIle----- 554  
Db 1557 CGTGAAGTGTGATGAAATTAATTAATTTGCTCCATGCTTATATAGGGCTCTTCTTACCCC 1616  
Qy 555 -----ArgSerLeuAla1 559  
Db 1617 TGTAATCTGTCAGTTGAGATCATGACAAACAACAATCTTTTGAACGAACCAATCTGT 1676  
Qy 559 ePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAsp-----GlnLeuAr 577  
Db 1677 TTTCTCTTTTCATCTGAGCCTTTATATATGTTCTCAAAATCAGAGTGTTCATTTCAA 1736  
Qy 577 gMetLeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAs 597  
Db 1737 ATTACTCAAGTCTTGGAGCTGAGA-----CACAGACAGATTGA 1775  
Qy 597 p-----ArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSe 613  
Db 1776 TGTGTTTCCCTCGAGAGATCTAAAGCCTCATCTGTTGAGGTACCTATCATTTG---TTCA 1832  
Qy 613 tSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAs 633  
Db 1833 CTATGGGAATTTTCATGCTTCCAGAAATTTTCAGGTTATGGAATCTGCAGACATTCAT 1892  
Qy 633 nMetPro-----SerThrTyrIleAlaLeuProSerGluIleSerLysLeuGlnCy 651  
Db 1893 TGTTCAACGGTTTCGATCAGATATAATATTTTCTGAGGAATTTGGGAATTAATGCA 1952  
Qy 651 sLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisAr 671  
Db 1953 ATTAAGGCATCTTAAA-----CTGCCAGATTTTATTGGCCA----- 1989  
Qy 671 oMetLysCysIleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerAr 691  
Db 1969 -----GTTGCCAGATTTTATTGGCCA----- 1989  
Qy 691 gAspAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGl 711  
Db 1990 -----GATTGCCCAAGTGG 2003  
Qy 711 uSerIleGlyValLysValProLysGlyIleGly-----LysLeuArgAspLeuGlnVal 730  
Db 2004 ATCT-----GTTCAACAAAGGAAGGCACTTGGATTTTCAAACTTCAAACTAT 2051  
Qy 730 uGluTyrValAspIleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSe 750  
Db 2052 TTCTTACTTGTCTCCAGTTGTTGCAGAGGAGGTTATT-----ATGGGG---ATTCA 2102  
Qy 750 rLysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLe 770  
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Qy 770 uTyrAlaAlaIleLysLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyI1 790  
Db 2140 -----GACTATAAAGTTT 2153  
Qy 790 eSerAspClyGly-----ThrLeuGluCysLeuAspSe 801  
Db 2154 TGGGACTCTGGGCTTCCCAACAATCTTGTCTATCTGCAGCAACTTGAATATTGAGTCT 2213





CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/930.996A  
 FILING DATE: 09-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/05272  
 FILING DATE: 15-APR-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 113.373  
 FILING DATE: 13-APR-1995  
 INFORMATION FOR SEQ ID NO. 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4465 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 204...3923  
 US-08-930-996A-3

Alignment Scores:  
 Pred. No.: 1,28e-57 Length: 4465  
 Score: 607.50 Matches: 249  
 Percent Similarity: 41.9% Conservative: 183  
 Best Local Similarity: 24.2% Mismatches: 388  
 Query Match: 11.5% Indels: 211  
 DB: 3 Gaps: 42

US-10-656-394A-8 (1-1032) x US-08-930-996A-3 (1-4465)

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 Qy 23 AlaAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTrpTyrIleLys 42  
 Db 267 AGCGTTGCTCTCAACGGTGATCTGCTCAACATGTTTCGGAAGCATAGGATCATGTTAAG 326  
 Qy 43 AspGluLeuLysThrMetClnAlaPheLeuArgAlaAlaGluLeuMetLysLysLysAsp 62  
 Db 327 ---CTCTTAAGAAGCTGAAATGATCTTGGCTGGTATTGAGATTGCTTAAGTATGCA 383  
 Qy 63 GluLeuLysValTrpAlaGluClnIleArgAspLeuSerTyrAspIleGluAspSer 82  
 Db 384 GAGATAAGCAAGCATCAATCCATCTGTGAGAGACTGGCTTAATGAGCTTCGAGATGCT 443  
 Qy 83 LeuAspGluPheLysValHisIleGluSerClnThrLeuPheArgGlnLeuValLysLeu 102  
 Db 444 GTCGACTCTGCTGAAATTTAATAGAAGAGCAATTAATGAGCTTGAAGCTTGAAGTG 503  
 Qy 103 ArgGluArgHisGileAlaIleArgIleHisAsn----- 114  
 Db 504 GAAGGTCAGCATCAGACACTTTTCAGAAACAGCAACCAAGCAAGTATGATGATGATTTTC 563  
 Qy 115 -----LeuLysSerArgValGluGluValSerSerArgSerThrArg 128  
 Db 564 CTTAACAATAAGCAAGTTGGAAGACACTATTGAACATTAAGGATTTGCAAGAGCAA 623  
 Qy 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148

Db 624 ATTGGTCTCCTT-----GGCTTAAAGGAGTATTTCATTCCAGAACTA 668  
 Qy 149 AspIleArgAsnGlnSerAlaArgAsnValAspGluAlaGluLeuValGlyPheSerAsp 168  
 Db 669 GAACTAGACACACCTTCAACTCTTTGATGATGAACCAAGATATCTTTGGT----- 719  
 Qy 169 SerLysLysArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAla----- 186  
 Db 720 AGCGAGAGCAANTAGAGGATTTGATGACCGTCTATTGCTGAAGGTCAAGTGGGAA 779  
 Qy 187 -----LysValIleCysValValGlyMetGlyGlyLeuGlyLysThrAlaLeuSerArg 204  
 Db 780 AATCTGACAGTGGTCTCTATTGTTGGAATGGGTGGCTTGGGCAAGCAACACTTGTCTAAA 839  
 Qy 205 LysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAlaIleThr 224  
 Db 840 GCCGTATATC-----AATGATGAGAGTGTGAAGAACATTTGATTTGAAAGCTGGTTTGT 896  
 Qy 225 ValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeuGly 244  
 Db 897 GTTTCGAGGCGTATATGCTTTTCAGAAATAACAAAGGGTTACTTCAAGAAATTTGGCTCA 956  
 Qy 245 ProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysValValGlnValHis 264  
 Db 957 ATTGACTTATGTTGATGACATCTTTAATCAGCTACAGTCAAA----- 998  
 Qy 265 HisLeuSerGluTyrLeuIleGluGluLeuLysArgTyrPheValValLeuAsp 284  
 Db 999 -----TTGAAGGAAGATTTAAGGAAAGAGTTTCTTATCGTCTCGGAT 1043  
 Qy 285 AspLeuTrp-----IleLeuHisAspTrpAsnTrpIleAsnGluLeuAlaPheProLys 302  
 Db 1044 GATGTGGAGATGACAACTACAGAGTGGAGTGAATTTGAGAAATGTTTGTGA----- 1097  
 Qy 303 AsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAlaGluLys 322  
 Db 1098 CAAGGAGATATAGGAAGTAAAGTATCTTGTGACGACGCAAGACAGAGTGTGCTTGATG 1157  
 Qy 323 CysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThr 342  
 Db 1158 ATGGGAATGAGCAAAATTT-----AGCATGGGCAATTTGTCACCGAAGCCTTCTGGTCT 1211  
 Qy 343 LeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGln 362  
 Db 1212 TTATTTCAAGACATGATGCTTGAAGAAACATGATGCTCTATG---GGACATTGGGAACCTGAA 1268  
 Qy 363 LysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIle 382  
 Db 1269 GAGGTTGGAAGCAAAATTTGACGCTAAGTGAAGGAGCTGCCCTTAGCTCTGGAAGCGCTT 1328  
 Qy 383 GlyAlaValLeuAlaThrLys---GlnValSerGluTrpGluLysPheTyrGluHisLeu 401  
 Db 1329 GCTGGCATGTTACGCTCCAAATCAGAGTGTGAAGAGTGGAAATGATTTCTGAGAAGTGA 1388  
 Qy 402 ProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGly 421  
 Db 1389 ATATGGGAGCTCGGAGACAATGACATATTACAGCGTTA-----ATGTTGAC 1436  
 Qy 422 TyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGlu 441  
 Db 1437 TACATGATCTCTCGCACATTTAAGCGATGCTTTCTTTTGTGCAATATTTCTCTAAA 1496  
 Qy 442 AspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArg 461  
 Db 1497 GATTATTCATTTAGGAAAGAACAAAGTTATTTCATCTATGATTTGCCAATGGTCTTTGTA--- 1553  
 Qy 462 ProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuAsn 481  
 Db 1554 CTTGTGGAAGATGAATAATTCAGATTTAGGCAACCAATTTCTTTCTCGAGTTGAGTTCA 1613  
 Qy 482 ArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys---Arg 500  
 Db 1614 AGATCATTATTGGAAGGGTCCCAATCTCTTCTGAAGGAACATAAAGGAATTTATTCCTA 1673



QY	501	IleHisAspIlelleAeArgAspIleThrValSerIleSerArgGlnGluAsnPhValLeu	520
Db	1674	ATGCATGACCTTGTCAATGATTTA--GCCCAACTTGCATCTTCAAACACTTGTATCAGG	1730
QY	521	LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis	540
Db	1731	TTGGAAGAGAGCCAGGAGATCTCATATGTTG--GAACAATGTGGCACTTATCATAT--	1784
QY	541	GlySerMetSerCysLysThrGlyLeuAsp--	553
Db	1785	---TCTATGGGATATGACGGTGGTGTGGAGAAATTGACACCCCTCTACAAATTGGACGAG	1841
QY	554	IleArgSerLeuAla--	565
Db	1842	CTGAGGACATTTGCTTCGACATGTAGTAGTGCAATTATTTCTATAACCCCTCTAACCAAG	1901
QY	566	SerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAspLeuGlu	585
Db	1902	AGGGTGTGGCATAACATACTGCCT--ACACTAAGATCCTTAAAGGCACTTATCATTTGCT	1958
QY	586	AspValThrPheLeuIleThrGlnLysAaspPheAspArgIleAlaLeuLeuCysHisLeu	605
Db	1959	CAT-----TACAAGATGGAGGAGTGCACCAATGACTTGTATTATCAAAATTAAGCTCCTC	2012
QY	606	LysTyrlLeuSerIleGlyTyrlSerSerSerIleTyrlSerLeuProArgSerIleGlyLys	625
Db	2013	AGATTTTTGGGATATTTCT--CGGACAAATATTAAGAGGTGGCCAGATTCCTATTGTGTG	2069
QY	626	LeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrlleAlaAlaLeuProSerGlu	645
Db	2070	TTGTATAACTTGGAGACATTCCTCTTTCATCTTGTAACCTTGAGGAGCTACCGCTCGAG	2129
QY	646	IleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrlAspAsn	665
Db	2130	ATGGAGAAGTTG-----ATTAACTTCGCTCATCTTGAC--	2162
QY	666	PheSerLeuAsnHisProMetLysCysIleThrAsnThr-----IleCysLeuProLys	683
Db	2163	-----ATAAGCAACACTTGGCACTTGAAGATGCCA--	2192
QY	684	ValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMet	703
Db	2193	-----CTACATCTG	2201
QY	704	AlaThrLysSerCysTyrSerGluSerIleGlyValLysValProLysGlyIleGlyLys	723
Db	2202	AGCAGTGTGAAAAGCCTCCAAAGTGTGGTGGGAGCCAAAGTTTCTGTAGGTGTTTGAGA	2261
QY	724	LeuArgAspLeuGlnValLeuLeuTyrlValAspIleArgArgThrSerSerArgAlaIle	743
Db	2262	ATGGAAGATTG-----GGTGAAGCACAA	2285
QY	744	LysGluLeuGlyGlnLeuSer-----LysLeuArgLysLeuGlyValThrThrAsnGly	761
Db	2286	AACTTATATGATCTCTATCAGTTGTAAAGTTGGAAAATGTG--GTTGATAGAGGGAA	2342
QY	762	SerThrLysGluLysCysLysIleLeuTyrlAlaAlaIleGluLysLeuSerSerLeuGln	781
Db	2343	GCTGTGAAGCCAAAGATGAGG-----GAG	2366
QY	782	SerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAspSer	801
Db	2367	AAGAAATCATGTTGAGCAATTA-----TCATTGGAGTGGAGTGAAGC	2408
QY	802	IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIle-----	817
Db	2409	ATTAGTCTGCATTTTCAAAACAGAAAGACATCTTGATGACTACGCCCATATAA	2468
QY	818	---LeuGluGluMet-----ProAsnTyrIleGlu	826
Db	2469	AATATTCAGAAGTCAAAATCATTTGGATATAGAGGGACAAACTTTTCCCAATTTGGGTAGCT	2528

RESUM.T 13

RESULT 13  
IIS-09-004-838-1

US-09-004-838-1  
: Sequence 1 Application US/09004838

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; Sequence 1, Application
: Data Set No 63500000

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Patent No. 6350933

; GENERAL INFORMATION:

APPLICANT: Michelmore, R

APPLICANT: Shen, Kathy

APPLICANT: Meyers, Blake

**TITLE OF INVENTION:** Procedures and Materials for

TITLE OF INVENTION:	FL
TITLE OF INVENTION:	Co

TITLE OF INVENTION: CONFERRING FRET RESISTANCE  
 :  
 NUMBER OF SEQUENCES: 140

NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:

CORRESPONDENCE: T. ADDRESS: T.

ADDRESSEE: T

STREET: TWO Emb

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

REF. 04111-0034  
; ;  
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy di

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: p

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; SOFTWARE: PatentIn Release #1.0,
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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/004,838

FILING DATE: 09-JAN-1998

CLASSIFICATION: 800

CLASSIFICATION: 800  
PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: US 08/781,734  
 ; APPLICATION NUMBER:

APPLICATION NUMBER: US 08/  
FILING DATE: 10-JAN-1997

10-JAN-1997  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER



QY	570	AlaValCysProAspGlnLeuArg-----MetLeuArgValLeuAspLeuGluAsp	586
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QY	587	ValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLys	606
DB	2860	-----ATTRRTCTT-----	2868
QY	607	TyrLeuSerIleGlyTyrSerSerSerSerIleTyrSerLeuProArgSerIleGlyLysLeu	626
DB	2869	-----AYAAATASRYAGGTACCARAATCGTGGGTAGTAGTATG	2904
QY	627	GlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAlaLeuProSerGluIle	646
DB	2905	AASCACTTGGCGTATCTTAATCTATCAGAACTTAAATCAACMCATTTACCGAAATATKTC	2964
QY	647	SerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPhe	666
DB	2965	TGCAATCTTTATATTAATTTACARACCCCTGATTGKTCTGGCTGTGAMTAT-----	3012
QY	667	SerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysValPheThr	686
DB	3013	-----TTAGTTAAKTTGCCCAARACCTTCTCA	3039
QY	687	ProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLys	706
DB	3040	AASCTT-----AAAAATTTGCASCATTTCATGATGGGTACT	3078
QY	707	SerCysTrpSerGluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAsp	726
DB	3079	CKAAKTTTAAAR-----AACATGCGCCCTTARGGATTTGGTGARTTTGAAAAART	3123
QY	727	LeuGlnValLeu-----GluTyrValAspIleArgThrSerSerArgAlaIleLysGlu	745
DB	3124	CTACAACTCTCTTNGTACATTCGATAGCAATAACGAGCTTAAGACTTCGAAAY	3183
QY	746	Leu-----GlyGlnLeuSerLysLeuArgLys-----LeuGlyValThr	758
DB	3184	CTCATGGGAARTTTGTATTTGTCGGCGCTGGGAAAAATGGAAAAATCGMGTGGATGCACG	3243
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QY	785	ValAspAlaAlaGlyIleSerAspGlyThrLeuGluCysLeuAspSerIleSerSer	804
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QY	805	ProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp	824
DB	3379	AAAAAACCCANAT-----ATGCTATAGGGGGTATA-----GAGTTCCANATGG	3426
QY	825	IleGluGlnLeuThrHisLeu-----LysLysIle	834
DB	3427	GTTGGTTNCATAAGGGTTCTTGAAACTAGAGATGTGTTATGTTGATGATAAGAAAGANTG	3486
QY	835	TyrLeuLeuArgSerLysLeuLysGlu-GlyLysThrMetLeuIleLeuGlyAlaLeuPr	854
DB	3487	TTTTACGTAGTTTCATCATCACCAGTGGGAATAGATGATATTTTCAGGGCYTACTGA	3546
QY	854	oAsnLeu-----MetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyLysIle	871
DB	3547	TGAGATGTGGAGAGGTATGATA-----GGGTNTCTTTGGGGCGGTAGA	3588
QY	871	uValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspG1	891
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QY 911 YGluCyAArgLeuGluSerGlyIleThrGlyIleHisLeuProLysLeuLysGlu 930
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RESULT 14
US-09-004-838-70
; Sequence 70, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 021070-078810US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4163 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4163
; OTHER INFORMATION: /note= "RLGI-E169"
US-09-004-838-70

Alignment Scores:
Pred. No.: 3,43e-56 Length: 4163
Score: 594.50 Matches: 265
Percent Similarity: 39.5% Conservative: 187
Best Local Similarity: 23.1% Mismatches: 373
Query Match: 11.3% Indels: 320
DB: 3 Gaps: 48

US-10-656-394A-8 (1-1032) x US-09-004-838-70 (1-4163)

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Db 1099 ATGGCGAATCGTCTCTTTCTGCGCTCTTTGACAGTGTG-----TTTGAAAAGCTG 1149
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QY 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTrpTyr 40
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Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60
Db 1210 TTGAAGGACACATTAGACCAAAATCCAGATCTGCTTAACGATCTCTCCCAAGGAAGATGA 1269
Qy 61 LysAspGluLeuLysValTrpAlaGlnIleArgAspLeuSerTrpAspIleGlu 80
Db 1270 ACTAATGAAGCCGTTAAAGAGTGGCTGAATGATCTCAACATTGGCTTATGACATAGAC 1329
Qy 81 AspSerLeuAspGluPheLysValHisIle 90
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Qy 91 GluSerGlnThrLeuPheArgGlnLeuVal 105
Db 1390 GGCCTCTCCAGTATGGTAAGAAACTAATCCAAAGTTGGTGCACAAATTTCTCACAAAGT 1449
Qy 106 HisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGluGluVal 123
Db 1450 AATAGGATGCATGCCAAGTTAGATGATATGCCACCAAGTTTACAAGAACTGGTAGAGGCA 1509
Qy 124 SerArgAsnThrArgTyrSerLeuVal 140
Db 1510 AAAAAATAATCTTTGGTTTAAGTGTGATACATATGAAAAAGCCA 1551
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160
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Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetLysPheThrAsn 180
Db 1588 AGCGGTACTCTCGGACGTGACAGATGATAAGAAAAAATTCGTGGAAGAGCTGTGTGGGGAT 1647
Qy 181 AlaAsnAspGlyProAlaLys 197
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Qy 198 GlyLysThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPhe 217
Db 1708 GGTAAACCAACTCTAGTAGACTTTTGTATGAT-----GAAAGAAAGTGAAGGATCACTTC 1764
Qy 218 ProCysAsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysLysAsp 237
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Db 2080 CTATCAAGATGATGCTTTGCTTTGTTGCTCAA-----CAGCATTT 2124
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Qy 799 LeuAspSer----- 801
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Qy 802 ----- 805
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Qy 806 ProPro-LeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp-- 824
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Qy 825 -----IleGluGlnLeuThrHisLeuLysLysIle----- 834
Db 3514 AGTATGATAGGTTNTCTGGGCGGTGAGAATAAGATCAATCTTGTGTAATGAAT 3573
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Qy 861 uTyrArgAsnAlaTyrLeuGlyGluLysLeu-----ValPheIly 874
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Qy 874 sThrGlyAlaPheProAsnLeuArg-----ThrLeuTrpIleTyrG1 888
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Qy 922 ----IleIleHis-----LeuProLysLeuLysGluIleProIleArgTyrGlySerIy 938
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Qy 961 tSerAspArgArg 965
Db 4099 AACAGATCGAAGG 4111

RESULT 15
US-08-930-996A-1
; Sequence 1, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 299..3958
; US-08-930-996A-1

Alignment Scores:
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Score: 580.50 Matches: 249
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Best Local Similarity: 24.5% Mismatches: 377
Query Match: 11.0% Indels: 207
DB: 3 Gaps: 44

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Db 362 AGGCTTGTCTCTTAATGTGTGATCTGCTCAACATGTTTTCGGAAGCATACAGATGATGTTGAG 421
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Qy 558 AlaIlePheGlyAspArg-----563  
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Qy      745 GluLeuGly-GlnLeuSerLysLeuArgLysLeuGly-----ValThrThrAs 760
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Qy      760 nGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLe 780
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Qy      780 uGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAs 800
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Db      2633 -TTTCCAACTGGGTAGCTGATCCTTTGTTTAAAGCTGGTGCATTTGTATCTTAGAAA 2691
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Job time : 607 secs



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 9, 2006, 22:42:35 ; Search time 1638 Seconds  
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5210.011 Million cell updates/sec

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Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*  
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	5268	100.0	3099	8 US-10-656-394A-7
2	5039	95.7	9090	8 US-10-656-394A-13
3	4942.5	93.8	3276	6 US-10-352-179-92
4	4925	93.5	3096	6 US-10-352-179-88
5	4906	93.1	3099	8 US-10-656-394A-3
6	4906	93.1	3674	8 US-10-656-394A-16
7	4753	90.2	76272	6 US-10-352-179-83

8	4397.5	83.5	4596	7	US-10-437-963-37316	Sequence 37316, A
9	4241.5	80.5	2997	8	US-10-656-394A-11	Sequence 11, Appl
10	3664.5	69.6	2982	7	US-10-437-963-2483	Sequence 2483, Ap
11	3205.5	60.8	3220	6	US-10-352-179-90	Sequence 90, Appl
12	3136	59.5	4147	8	US-10-656-394A-5	Sequence 5, Appl1
13	3072	58.2	2982	8	US-10-656-394A-1	Sequence 1, Appl1
14	3068.5	58.2	2925	7	US-10-437-963-41016	Sequence 41016, A
15	3063.5	58.2	2940	6	US-10-352-179-84	Sequence 84, Appl
16	2814	53.4	2711	7	US-10-437-963-36603	Sequence 36603, A
17	2762	52.4	2422	8	US-10-656-394A-15	Sequence 15, Appl
18	2575	48.9	2982	6	US-10-352-179-86	Sequence 86, Appl
19	2539	48.2	3024	7	US-10-437-963-7778	Sequence 7778, Ap
20	2484.5	47.2	3492	7	US-10-437-963-49433	Sequence 49433, A
21	1902	36.1	2781	7	US-10-437-963-69440	Sequence 69440, A
22	1878.5	35.7	2439	7	US-10-437-963-74853	Sequence 74853, A
23	1722.5	32.7	2351	6	US-10-352-179-97	Sequence 97, Appl
24	1493	28.3	2265	6	US-10-352-179-96	Sequence 96, Appl
25	1384	26.3	1355	6	US-10-437-963-94753	Sequence 94, Appl
26	1238.5	23.5	2937	7	US-10-437-963-64619	Sequence 64619, A
27	1224	23.2	2967	7	US-10-437-963-54125	Sequence 54125, A
28	1211	23.0	4288	7	US-10-437-963-47020	Sequence 47020, A
29	1210	23.0	2946	7	US-10-437-963-32604	Sequence 32604, A
30	1209.5	23.0	4026	7	US-10-437-963-76118	Sequence 76118, A
31	1209	22.9	2928	7	US-10-437-963-55316	Sequence 55316, A
32	1187.5	22.5	4542	7	US-10-437-963-31644	Sequence 31644, A
33	1135	21.5	3455	7	US-10-437-963-88509	Sequence 88509, A
34	1101	20.9	3618	7	US-10-437-963-32912	Sequence 32912, A
35	1085.5	20.6	2325	7	US-10-437-963-88300	Sequence 88300, A
36	1078	20.5	2799	7	US-10-437-963-12196	Sequence 12196, A
37	1077.5	20.5	2844	7	US-09-354-453-35	Sequence 35, Appl
38	1062.5	20.2	2862	3	US-10-267-718-35	Sequence 35, Appl
39	1062.5	20.2	2862	3	US-10-267-718-35	Sequence 35, Appl
40	1048	19.9	3495	7	US-10-437-963-67624	Sequence 67624, A
41	1034.5	19.6	2954	3	US-09-354-453-34	Sequence 34, Appl
42	1034.5	19.6	2954	3	US-10-267-718-34	Sequence 34, Appl
43	1034.5	19.6	6760	3	US-09-354-453-33	Sequence 33, Appl
44	1034.5	19.6	6760	3	US-10-267-718-33	Sequence 33, Appl
45	1025	19.5	2631	7	US-10-437-963-67623	Sequence 67623, A

## ALIGNMENTS

RESULT 1  
US-10-656-394A-7  
; Sequence 7, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3099)  
US-10-656-394A-7

Alignment Scores:  
Pred. No.: 0  
Score: 5268.00  
Length: 3099  
Matches: 1032  
Percent Similarity: 100.0%  
Conservative: 0  
Best Local Similarity: 100.0%  
Mismatch: 0  
Query Match: 100.0%  
Indels: 0  
DB: 8  
Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-7 (1-3099)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
Db 1 ATGCGGAGAGCGGTGCTGAGCATGGCGAGGTGCTGCTGGCGACGCGCATCAGCAAGGCC 60  
Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluIysAspIleThrPyr 40  
Db 61 GCCTCGCTGCTGCGACGAGACCGCCTCTGCTGGCGTTCGAGAAAGACATCTGGTAT 120  
Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysIys 60  
Db 121 ATCAAAGATGAGCTAAACACGATGCAAGCATTCCTTAGAGCTGCTGAATCTATGAAAAAG 180  
Qy 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTrpIleGlu 80  
Db 181 AAGATGAATTAATAAGTTTGGCAGAGCAATATGCTGACCTGCATATGACATGAA 240  
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 241 GATTCCCTTGATGAATTTAAGGTCCATATTGAAAGCCAAACCCCTATTTCGTGAGTTGGTG 300  
Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisIleLeuLysSerArgValGlu 120  
Db 301 AAATCAGAGAAGCCACCGAATGCTATCCGTATCCACAACTTAAATCAAGAGTTGAA 360  
Qy 121 GluValSerSerArgAsnThrArgTyxSerLeuValLysProIleSerGlyThrGlu 140  
Db 361 GAAGTGAGTAGCAGGAACACACGCTACAGTTTGTAGTCAAGCTTATTTCTCTGCGACAGAG 420  
Qy 141 IleAspMetAspSerTyxAlaGluAspIleArgHisGlnSerAlaArgAsnValAspGlu 160  
Db 421 ATTGACATGATTCCTATGCAAGACATTCGTATCAGTCAGCTCGCAATGTGGATGAG 480  
Qy 161 AlaGluLeuValGlyPheSerAspSerLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 481 GCTGAGCTGTTGGGTGTTCTGACTCCAAGAAAGGCTGCTGAAATGATGATACCAAT 540  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 541 GCTAATGATGGTCCGGCCAAAGTAAATCTGTGTTGGGATGGGTGTTTAGCAAGACA 600  
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 601 GCTCTTTGAGGAAGATCTTTGAAAGCGAGAGACATAGGAAGAACTTCTCTTGCAAT 660  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 661 GCTTGATTTACAGTGTCAATCATTTTACAGGATGAGCTACTTAAAGATATGATACGC 720  
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysValVal 260  
Db 721 CAACTTCTTGCCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCAGGAGAGTGGTG 780  
Qy 261 ValGlnValHisIleSerSerGluTyxIleIleGluLeuLysGlyLysArgTyxPhe 280  
Db 781 GTGCAAGTACATCATCTTCTTGAGTACTGATAGAAGAGCTCAAGGAGAAGAGTACTTT 840  
Qy 281 ValValLeuAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 841 GTTGTCTAGATGATCATGATTTTACATGATGGATGGATTTGATTAATGAATTCATTT 900  
Qy 301 ProLysAsnAsnLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
Db 901 CCTAAGAACAATAAGAGGGGAGTCGAATAGTAAATACCACTCGGAATGTTGATCTGCG 960  
Qy 321 GluLysCysAlaThrAlaSerLeuValTyxHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 961 GAGAAGTGTGCACAGCTCATCTGGTGTACCACTTGTATTTCTTGCAAGTACAGATGCC 1020  
Qy 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1021 ATAACTTGTCTAGAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAATAAAAAAT 1080

Qy 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1081 ATGCAAAAAGATGGTGAACGAATTTAAATTAATTTGGTGGTCTACCATTTAGCAATACTT 1140  
Qy 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyxGluHis 400  
Db 1141 ACNATGAGAGCTGTGCTTGCACACTAAACAGGTGTCAGAAATGGAGAAATTTCTATGACAC 1200  
Qy 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu 420  
Db 1201 CTTCTCTCAGAACTAGAAATAAAACCAAGCCTGGAAGCTTTTGAGGAGAATGGTGACCTA 1260  
Qy 421 GlyTyxAsnHisLeuProSerHisLeuLysProCysPheLeuTyxLeuSerIlePhePro 440  
Db 1261 GGTATCAACACCTACCTCCATCCCATTTTGAACCAACATGCTTTTGTATCTTAAGTATCTTTCT 1320  
Qy 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGATAGCAGAAAGGTTTCTT 1380  
Qy 461 ArgProLysValGlyMetThrThrLysAspValGlyLysTyxPheAsnGluLeuIle 480  
Db 1381 AGACCAAGGTGGGATGACGACTAAGGATGTCGGAAGAAAGTACTTTTAATGAGCTAATC 1440  
Qy 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1441 AACCGAAGTATGATTCAACGATCAAGAGTGGCGATAGCAGGAGGAAAAATTAAGACTTGTGGA 1500  
Qy 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeu 520  
Db 1501 ATTCAATGATATCATCGGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTA 1560  
Qy 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
Db 1561 TTACCAATGGAGATGGCTCTGATTTAGTTTACGAGGAAACACTCGGCACATAGCATTTCCAT 1620  
Qy 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleAspSerLeuAlaIlePhe 560  
Db 1621 GGGAGTATGCTCGCAAACTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 1680  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1681 GGTGACAGACCAAGAGTCTAGCACATGTCAGTTTGTCCAGATCAATTCAGGATGTTACGG 1740  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1741 GTCCTGGATCTTGAAGATGTGACATTTTAATCACTCAAAAAGATTTCCGACCGTATTGCA 1800  
Qy 601 LeuLeuCysHisLeuLysTyxLeuSerIleGlyTyxSerSerSerIleTyxSerLeuPro 620  
Db 1801 TTGTTGTGCCACTTGAATATCTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTT 1860  
Qy 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyxIleAla 640  
Db 1861 AGATCCCAATGGTAAACTTACAGGCGCTTACAACTTTGAAACATGCCGAGACACATACATGCA 1920  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1921 GCACCTCAAGTGCAGATCAGTAACTCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
Qy 661 PheHisTyxAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCys 680  
Db 1981 TTTCAATATGACAACTTTTGTCTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAATGC 2040  
Qy 681 LeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGlu 700  
Db 2041 CTGCTTAAAGTATTCACACTTTTAGTTCGGATGATCGTGCAAAACAAATTTGCTGAA 2100  
Qy 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
Db 2101 TTGCATGTCGCCCAACCAAGTTGCTGGTCTGAATCAATCAATCGGTGTGAAGGTACCCAAAGGA 2160  
Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyxValAspIleArgArgThrSerSer 740

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|||||
2161 ATAGTAAGTTGCGAGACTTGCAGGTTCTAGAGTATGATATCAGCGCGACCACTAGT 2220
QY |||||
741 ArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrAsn 760
Db |||||
2221 AGAGCAATCAAGAGCTGGGCGAGTTAAGCACTGAGGAAATAGGTGTGCAACAAC 2280
QY |||||
761 GlySerThrLysGluLysCysLysIleLeuTyAlaAlaIleGluLysSerLeu 780
Db |||||
2281 GGGTCGACAAAGGAAAAATGATATCTTTATGCGACCACTTGAAGAAGCTCTTCCCTC 2340
QY |||||
781 GlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAsp 800
Db |||||
2341 CAATCTCTCCATGTGGATGCTGCGAGAACTCTCAGATGGTGGCAACCTTGAGTGCTAGAT 2400
QY |||||
801 SerIleSerProProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 820
Db |||||
2401 TCTATTTCATCTCTCTCCCTACTCAGGACACCTCGTGTGGATGGAATCTTGGAGGAG 2460
QY |||||
821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyThrLeuArgSerLys 840
Db |||||
2461 ATGCTTAACGTGATTTGACACCTCCTCCTCAGTCTGAGAGAGATCTACTTATGAGGACAA 2520
QY |||||
841 LeuLysGluGlyLysThrMetLeuLeuGlyAlaLeuProAsnLeuMetValLeuHis 860
Db |||||
2521 CTAAAGGAAGGTAAACCATCTGATCTTGGGCGACTGCGCCCAACCTCATGTGCTTCAT 2580
QY |||||
861 LeuTyArgAsnAlaTyLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsn 880
Db |||||
2581 CTTTATCGGAATGCTTACCTTGGGGAAGCTAGTATTTCAAAACAGAGCATTTCCCAAT 2640
QY |||||
881 LeuArgThrLeuTrpIleTyGluLeuAspGlnLeuArgGluIleArgPheGluAspGly 900
Db |||||
2641 CTTAGACACCTTGGATTTATGAATTTGATCAGTCAAGAGAGATCAGATTTGAGGACGCG 2700
QY |||||
901 SerSerProLeuGluLysIleGluIleGlyCysArgLeuGluSerGlyIleThr 920
Db |||||
2701 AGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTGGAACTCGGATTAAT 2760
QY |||||
921 GlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyGlySerLysValAla 940
Db |||||
2761 GGTATCAATTCACCTTCCAAAGCTCAAGGAGATTCCTAATAGATACGGAAGTAAAGTGCT 2820
QY |||||
941 GlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMet 960
Db |||||
2821 GGGCTTGGTCACTGGAGGAGAAAGTGAACGACACACCAATCGCCCGCTGTCTGCTAATG 2880
QY |||||
961 TySerAspArgArgTyHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluVal 980
Db |||||
2881 TACAGTGACCGAAGGTATCAGACCTGGGGGCTGAAGCGCAAGATCTTCTATAGAGTG 2940
QY |||||
981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000
Db |||||
2941 CAAACAGCAGATCTCTGTTCTGATGCCGAGGATCAGTCACTATGACGTGGAAGCAACG 3000
QY |||||
1001 AspProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeuThrThr 1020
Db |||||
3001 GATCCCTTCCGACGACGAGGAGAGAGCTCGCAGTTCGAGTGATCAGTTGACGACG 3060
QY |||||
1021 AsnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032
Db |||||
3061 AATGATAGGAAGATAGGACACAGCTCAAGCTGGC 3096
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## RESULT 2

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US-10-656-394A-13
; Sequence 13, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE OF INVENTION: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
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; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 23216
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-13

Alignment Scores:
Pred. No.: 0 Length: 99090
Score: 5039.00 Matches: 983
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.7% Indels: 0
DB: 8 Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-13 (1-99090)

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Db 77635 TATATCAAGATGAGCTTAAACACGATGCAAGCATTTCTTAGAGCTGCTGAACCTTATGAA 77694
QY 60 LysLysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyAspIle 79
Db 77695 AAGAAAGATGACTTATTAAGGTTTGGCAGAGCAAAATACGTGACCTGTCTATATGACATT 77754
QY 80 GluAspSerLeuAspGluPheLysValHisIleGluSerGlnThrIleuPheArgGlnLeu 99
Db 77755 GAAGATTCCTTGTATGAATTTAAGGTCATATTGAAGCAAAACCCCTATTTCGTCAAGTTG 77814
QY 100 ValLysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgVal 119
Db 77815 GTGAACACTCAGAAACCCACCCGANTTGTATCCGTATCCACACCTTAATCAAGAGTT 77874
QY 120 GluGluValSerSerArgAsnThrArgTySerLeuValLysProIleSerSerGlyThr 139
Db 77875 GAAGAAAGTGAGTAGCAGAAACACACGCTACAGTTTAGTCAAGCCCTATTTCCTCTGGCACA 77934
QY 140 GluIleAspMetAspSerTyAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159
Db 77935 GAGATTGACATGGATTCTCTATGCAAGAGACATTCGTAAATCAGTCAGCTCGCAATGTGAT 77994
QY 160 GluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuGluLeuMetIleAspThr 179
Db 77995 GAAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATATGATCGATACC 78054
QY 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLys 199
Db 78055 AATGCTAATGATGTCCGCGCAAGGTAACTGTGTGTGGATGGGTGGTGTAGGCAAG 78114
QY 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219
Db 78115 ACAGCTCTTTCGAGAAAGATCTTTGAAGCGCAAGAGACATTTAGGAAGAACTTCCCTTGC 78174
QY 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239
Db 78175 AATGCTTGATTTACAGTGTCAATATNTTTCACAGGATTTGAGCTACTTAAAGATATGATA 78234
QY 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysVal 259
Db 78235 CGCCAACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTGAAGCAAGATTTGCAAGGAAGGTG 78294
QY 260 ValValGlnValHisLysLeuSerGluTyLeuIleGluLeuLysGlyLysArgTy 279
Db 78295 GTGGTCAAGTACATCATCTTCTGAGTACTGTAAGAGCTCAAGGAGGAAGAGGTAC 78354
QY 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299
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Db 78355 TTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAATGAAATTCGA 78414  
Qy 300 PheProLysAsnAsnLysGlySerArgileValIleThrThrArgAsnValAspLeu 319  
Db 78415 TTTCTCTAAGACAATAAGAGGCGACATGCAATAGTAATAACCACTCGGAATGTCATCTT 78474  
Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyRhiSleuAspPheLeuGlnMetAsnAsp 339  
Db 78475 GCGAGAGTGTGCGACAGCTCTACTGTGTGTACCTTGTATTTCTTGAGATGACGAT 78534  
Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
Db 78535 GCCATAACATTGCTACTCGAGAAAACAAATAAATAAATCATGACACATGGAATCAATAAA 78594  
Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
Db 78595 AATATGCCAAAAGATGGTGAACGAATGTAAATAATGTGTGTCTTACCAATAGCAATA 78654  
Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyRglu 399  
Db 78655 CTTACAAATAGGAGCTGTGCTGCAACTAAACAGGTGTGCAATGGGAGAAATTCATGAA 78714  
Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThr 419  
Db 78715 CACTTCTCTCGAAGTAAATAAACCAGCTGGAAGCTTTGAGGAGAAATGCTATCTT 78774  
Qy 420 LeuGlyTyRAsnHisLeuProSerHisLeuLysProCysPheLeuTyRLeuSerIlePhe 439  
Db 78775 CTAGGTTACAACCCACTACCATCCATTTGAAACCATGCTTTTGTATCTAAGTATCTT 78834  
Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
Db 78835 CCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATGGAATGCAAGGGTTT 78894  
Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyLysSerTyRAsnGluLeu 479  
Db 78895 GTTAGACCAAGGTTGGATGACGACTAAGGATGTCGAGAAAGTTTACTTTAATGAGCTA 78954  
Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
Db 78955 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGATGCGGCAAGAAATTAAGACTGT 79014  
Qy 500 ArgIleHisAspIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
Db 79015 CGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGACAGCAAGAAATTTGTA 79074  
Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
Db 79075 TTATTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAACATCGCCACATAGCATTC 79134  
Qy 540 HisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
Db 79135 CATGGGAGTATGCTCTGCAAACTGGATTTGGATTTGGAGCAATTTATTCATCATAGCTATT 79194  
Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
Db 79195 TTTGTGTACAGACCCAGAGCTAGCACATGCGAGTTTGTCCAGATCAATTTGAGGATGTA 79254  
Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
Db 79255 CGGGTCTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATT 79314  
Qy 600 AlaLeuLysCysHisLeuLysTyRLeuSerIleGlyTyRSerSerSerIleTyRSerLeu 619  
Db 79315 GCAITGTTGTGCCACTTGAAATCTTGAGTATTGGATATTCGTCTATCCATATATTCACTT 79374  
Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyRile 639  
Db 79375 CCCAGATCCATTTGTTAACTACAGGGCTACAACTTTGAAATGCGCGACACATACATT 79434  
Qy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659  
Db 79435 GCAGCAGCTACCAAGTGAGATCAGTAAATCTCCAATGTCTGACTACTCTTCTGTTGTATAGGA 79494

Qy 660 GlnPheHisTyRAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 79495 CAGTTTTCATATATGACAACTTTAGTCTAAACCCCAATGAAGTGAATCAATAACAATA 79554  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAla 699  
Db 79555 TGCCTGCCCTAAAGTTATTCACACCTTTAGTTAGTTCGCGATGATCGTGCAGAAACAAATTCCT 79614  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 79615 GAAATTGCACATGGCCACCAAAAGTTGCTGCTCTGAATCAATCGGTGTGAAGTACCCAAA 79674  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyRValAspIleArgArgThrSer 739  
Db 79675 GGAATAGTAGTAAAGTTGCGAGACTTTCAGGTTCTAGAGTATGATAGTATCAGGCGHCCAGT 79734  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThr 759  
Db 79735 AGTAGAGCAATCAAAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGACACA 79794  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyRAlaAlaIleGluLysLeuSerSer 779  
Db 79795 AACGGTGCAGCAAGGAAATGTTAGATACCTTTATGACGCCATTTGAGAGCTCTCTTCC 79854  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799  
Db 79855 CTCCAAATCTCTCCATGTGGATGCTGCGAGGAATCTCAGATGTTGGAACACTTTGAGTGCCTA 79914  
Qy 800 AspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 819  
Db 79915 GATTCTATTTCT 79974  
Qy 820 GluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyRLeuLeuArgSer 839  
Db 79975 GAGATGCTTAACCTGGATTGAGCAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 80034  
Qy 840 LysLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeu 859  
Db 80035 AAATTAAGAGAGGTAAACCATGCTGATCTCTGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGT 80094  
Qy 860 HisLeuTyRArgAsnAlaTyRLeuGlyLysLeuValPheLysThrGlyAlaPhePro 879  
Db 80095 CATCTTTATCGAATGCTTACCTTTGGGAGAGAGCTAGTATTTCAAAACAGGAGCATTTCCA 80154  
Qy 880 AsnLeuArgThrLeuTrpIleTyRLeuAspGlnLeuArgGluIleArgPheGluAsp 899  
Db 80155 AATCTTAGAACACTTTGGATTTATGAATTTGATGATGATGATGATGATGATGATGATGATGAT 80214  
Qy 900 GlySerSerProLeuLeuGluLysIleGluIleGlyGlyCysArgLeuGluSerGlyIle 919  
Db 80215 GGCAGCTCACTCTGTTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGAATCTGGGATT 80274  
Qy 920 ThrGlyIleIleHisLeuProLysLeuLysGluIlePheProIleArgTyRLeuSerIleVal 939  
Db 80275 ACTGGTATCATCTCACTTCCAAAGCTCAAGGAGATTTCCAAATTTAGATAGCGAAGTAAAGTG 80334  
Qy 940 AlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeu 959  
Db 80335 GCTGGGCTTGGTTCAGCTGGAGGAGAGTGAACGACACACCCCAAAATCGCCCGTCTGCTA 80394  
Qy 960 MetTyRSerAspArgArgTyRHisAspLeuGlyAlaGluAlaGluGlySerSerIleGlu 979  
Db 80395 ATGTACAGTACCGAAGGATCACGACCTGGGGGCTGAAGCGAAGGATCTCTTATAGAA 80454  
Qy 980 ValGlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAla 999  
Db 80455 GTGCAAAACACAGATCTCTGTCTCTGATGCGAAGGATCAGTCACTGTAGTAGTGAAGCA 80514  
Qy 1000 ThrAspProLeuProGluGlnGluSerSerGlnSerGlnValIleThrLeuThr 1019  
Db 80515 ACGGATCCCTTCCCAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACGTTGACG 80574

QY 1020 ThrAsp 1022

Db 80575 ACGAATGAT 80583

# RESULT 3

US-10-352-179-92

; Sequence 92, Application US/10352179

; Publication No. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

; FILE REFERENCE: 2727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 92

; LENGTH: 3276

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3276)

; OTHER INFORMATION:

US-10-352-179-92

## Alignment Scores:

Pred. No.: 0 Length: 3276  
Score: 4942.50 Matches: 987  
Percent Similarity: 91.8% Conservative: 14  
Best Local Similarity: 90.5% Mismatches: 31  
Query Match: 93.8% Indels: 59  
DB: 6 Gaps: 1

US-10-656-394A-8 (1-1032) x US-10-352-179-92 (1-3276)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 1 ATGGCGGACGCTGCTGAGCATGGCGAGTGGCTGGTGGCGAGCGCCATCAGCAAGGCC 60  
QY 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTrp --- 39  
Db 61 GCCTCGGCTGCTGGCGAGCAGCAGCTCTGCTGGCGCTGGAGAAACATCTGGTAT 120  
QY 39 ----- 39  
Db 121 ATCAAGATGAGTTGAAATAATATGCGAGCATTCCTTAGAGCTGCGAAGTATGAAAAAG 180  
QY 39 ----- 39  
Db 181 AAAGACGAATATTAAAGTTTGGGCGAGCAAAATACGTGCTGTTATATGACATTGAA 240  
QY 40 -----TyrIle 41  
Db 241 GATTCCTTGATGAATTTAAGTCCATGTTGAAAGTCAACCCCTATTTCGTGATATATC 300  
QY 42 LysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 61  
Db 301 AAAGATGAGCTAAACACGATGCAAGCATTCCTTAGAGCTGCTGAACTTATGAAAAAGAA 360  
QY 62 AspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAsp 81  
Db 361 GATGAATATTAAAGTTTGGCGAGCGCAATATGTCGCTGTCATATGACATTGAAGAT 420  
QY 82 SerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLys 101  
Db 421 TCCCTTGATGAATTTAAGTCCATATTGAAAGCCCAACCCCTATTTCGTGATTTGGTGA 480  
QY 102 LeuArgGluArgHisArgIleAlaIleArgIleHisLeuLysSerArgValGluGlu 121

Db 481 CTCAGAAACGCCACCGAATTGCTATCCGATATCCCAACCTTAATCAAGAGTTCAAGAA 540  
QY 122 ValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrIle 141  
Db 541 GTGAGTAGCAGGAACACACGCTAGCTTTAGTCAAGCCCTATTTCCTCTGGCAGAGATT 600  
QY 142 AspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGluAla 161  
Db 601 GACATGGATTCCTATGCGAAGACATTCGTATCACTAGCTCGCAATGTGATCAAGCT 660  
QY 162 GluLeuValGlyPheSerAspSerLysArgLeuLeuLeuMetLysThrAsnAla 181  
Db 661 GAGCTTGTGGTTCCTGCTCAAGAAAGGTCCTTGAATGATCATCAATCAATGCT 720  
QY 182 AsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThrAla 201  
Db 721 AATGATGGTCCGGCAAGTAATCTGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 780  
QY 202 LeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAla 221  
Db 781 CTTTCGAGGAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTTGCATGCT 840  
QY 222 TrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArgGln 241  
Db 841 TGGATTACAGTGTCAATCATTTACAGAGTTGAGCTACTCAAGATATGATAGCCCAA 900  
QY 242 LeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluGlnGlyLysValValVal 261  
Db 901 CTTCTAGTCCCAATTCCTGAAACAACTCTTCAAGAAATTTGCAAGGAAGGTGGTGGT 960  
QY 262 GlnValHisLeuSerGluTyrLeuIleGluLeuLysGluLysArgTyrPheVal 281  
Db 961 CAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGAGTACTTTGTT 1020  
QY 282 ValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhePro 301  
Db 1021 ATTCTAGATGATCTATGATTTTACATGATTTGCAATTTGCAATTTGCAATTTGCAATTT 1080  
QY 302 LysAsnAsnLysLysGlySerArgIleValIleThrArgAsnValAspLeuAlaGlu 321  
Db 1081 AAGAAACAATAAGAGGGCGATGCAATAGTAAATCAACCACTCGGAATGTTGATCTAGCGAG 1140  
QY 322 LysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIle 341  
Db 1141 AAGTGTGCCACAGCTCCTGCTGCTGATCCACCTGATTTCTTTCAGATGAACGATGCCATA 1200  
QY 342 ThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMet 361  
Db 1201 ACATTTGCTACTAAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAATAAAAATATG 1260  
QY 362 GlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThr 381  
Db 1261 CAAGAGATGTTGAACGATTTGTAATTAATGATGCTGCTACCATTTAGCAATATTACA 1320  
QY 382 IleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHisLeu 401  
Db 1321 ATAGGAGCTGTCTTGAACCTAAACATGCTGCTGCAATGGAGAAATTTCTATGAACAGCTT 1380  
QY 402 ProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGly 421  
Db 1381 CTTTCAAGACTAGAAATAAACCCCAAGCTCGAAGCTTTGAGGAGATGTTGACCCCTAGGT 1440  
QY 422 TyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGlu 441  
Db 1441 TACAACCACTACCATCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTCTCTGAG 1500  
QY 442 AspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArg 461  
Db 1501 GATTTTGAATCAAGAGGATCTCTGTTAGTAGATGATGATAGCAGAGAGGGTTGTTAGA 1560  
QY 462 ProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIleAsn 481  
Db 1561 CCGCAGGTGGGATGACGACTAAGGATGTCGAGAGAAAGTTACTTTAATGAGCTAATCAGC 1620

Qy 482 ArgSerMetIleClnArgSerArgValGlyIleAlaGlyIleLysThrCysArgIle 501  
Db 1621 CGAAGTATGATTAACAGATCAAGAGTGGGCATATCAGGAAATAAAGACTTGTGCAATC 1680  
Qy 502 HisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAenPheValLeuLeu 521  
Db 1681 CATGATATCATCGTGATATACAGTTTCATCTCGAGACAGGAAATTTTGTATGTTA 1740  
Qy 522 ProMetGlyAspClySerAspLeuValGlnGlnAenThrArgHisIleAlaPheHisGly 541  
Db 1741 CCAATGGGAGATGGCTCTGATTTAGTTTACGAAACACCTGCCACATAGCATTTCCATGGG 1800  
Qy 542 SerMetSerCysIleThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly 561  
Db 1801 AGTATGTCCTGCACAAACAGGATTTGGATTGGAGCATTTATCGATCAATTTTGGT 1860  
Qy 562 AspArgProIleSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgVal 581  
Db 1861 GACAGACCCCAAGATCTAGCACATGAGTTTGTCTAGATCAATTTGAGGATTTTACGGGTC 1920  
Qy 582 LeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 601  
Db 1921 TTGATCTTGAAGATGTGACATTTCTATCACTCAAAAGATTTGACGCTATTTGATG 1980  
Qy 602 LeuCysHisLeuLysThrIleSerIleGlyTrpSerSerIleThrValSerLeuProArg 621  
Db 1981 TTGTGACCTTGAAATATCTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2040  
Qy 622 SerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTrileAlaAla 641  
Db 2041 TCCATTTGTTAACTACAGGCTCTACAACTTTTGAACATGCTGAGACATACATTCGACGA 2100  
Qy 642 LeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPhe 661  
Db 2101 CTACCAAGTCAGATCAGTAAATCTCCAAATGCTGCATATCTCTCTGTTGATGAAAGTTT 2160  
Qy 662 HisTrpAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
Db 2161 GTTATGACACTTTAGTCTAAACCCCAATGAAGTGCATTAATCAACATATAGCTTG 2220  
Qy 682 ProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeu 701  
Db 2221 CCTAAAGTATTCACACCTTTAGTTAGTCCGATGATCGTCAAAACAAATTTGCTGAATG 2280  
Qy 702 HisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValPheLysGlyIle 721  
Db 2281 CACTGGCCACCAAGTTGCTGCTGATCATTCGTTGAGGTACCCAAAGAAATA 2340  
Qy 722 GlyLysLeuArgAspLeuGlnValLeuGluTrpValAspIleArgThrSerSerArg 741  
Db 2341 GGTAAAGTTCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA 2400  
Qy 742 AlaIleLysGluLeuGlyGlnLysSerLysLeuArgLysLeuGlyValThrThrAsnGly 761  
Db 2401 GCATCAAGACTGGGCACTTAAAGCAAGTTGAGGAATTTAGTGTGATTAACAAAGGC 2460  
Qy 762 SerThrLysGluLysCysLysIleLeuTrpAlaAlaIleGluLysLeuSerSerLeuGln 781  
Db 2461 TCGACAAAGGAAATGTAAGATATCTTTATGACGCCATTGAGAAGCTCTCTTCCCTCAA 2520  
Qy 782 SerLeuHisValAspAlaAlaGlyLysSerAspClyGlyThrLeuGluCysLeuAspSer 801  
Db 2521 TCTCTATGTGAATGCTGCGTTATTCAGATATTGAAACACTTGAAGTGTGATTTCTCTCTCT 2580  
Qy 802 IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluMet 821  
Db 2581 ATTATCATCT 2640  
Qy 822 ProAsnTrpIleGlnGlnLeuThrHisLeuLysLysIleThrLeuLeuArgSerLysLeu 841  
Db 2641 CCTAATGATTTGACAGCT 2700

Qy 842 LysGluGlyLysThrMetLeuIleLeuGlyAlaIleProAsnLeuMetValLeuHisLeu 861  
Db 2701 AAGGAAGGTAAACCATCTGATATCTTGGGGCATTTGCCAACCTCATGTGCTCTTTATCTT 2760  
Qy 862 TyrArgAsnAlaTrpLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsnLeu 881  
Db 2761 TATTGGAATGCTTACCTTGGGGAAGCTAGTATTCAAAACGGGAGCATTTCCCAATCTT 2820  
Qy 882 ArgThrLeuTrpIleTrpLeuLysGlnLeuAspGlnLeuArgLysLeuPheGluAspGlySer 901  
Db 2821 AGAACACTTCTGATTTTACGAATTGGATTCAGTCAAGAGATGAGATTTTGAAGATGGCAGC 2880  
Qy 902 SerProLeuLeuGluLysIleGlyGlyCysArgLeuGluSerGlyIleThrGly 921  
Db 2881 TCACCCCTGTTGGAAAAGATAGAAATCTCTTGTCTGAGGTTGGATTCAGGATTTATGTT 2940  
Qy 922 IleIleHisLeuProLysLeuLysGluIleProIleArgTrpCysSerLysValAlaGly 941  
Db 2941 ATCATTTCACTTCCAAAGCTCAAGGATTTCTTCAATACAAAGTAAAGTGGCTAGG 3000  
Qy 942 LeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyr 961  
Db 3001 CTTGTCTAGCTGGAGGAGAGTGAACACACACCCCAATCGCCCTGCTGCGAATGGAC 3060  
Qy 962 SerAspArgArgTrpHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGln 981  
Db 3061 AGTGACCGAAGGATTCAGACCTTGGGGCTTGAAGCCGAGGATCTTCTATAGAAGTGCAA 3120  
Qy 982 ThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThrAsp 1001  
Db 3121 ACAGCAGATCTCTTCTGATGCGAAGGATCAGTCACTGTAGCAGTGGAGCAACGAT 3180  
Qy 1002 ProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeuThrAsn 1021  
Db 3181 CCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGCAGTGCAGTGCAGTGCAGGAC 3240  
Qy 1022 AspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3241 GATAGCAGAGAGATAGGACACAGCTCAAGCTGGC 3273

## RESULT 4

US-10-352-179-88  
; Sequence 88, Application US/10352179  
; Publication No. US20040006788A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Guo-liang  
; APPLICANT: Liu, Guifu  
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl.  
; FILE REFERENCE: 22727/04108  
; CURRENT APPLICATION NUMBER: US/10/352,179  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/352,106  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 3096  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3096)  
; OTHER INFORMATION:  
US-10-352-179-88

Alignment Scores:  
Pred. No.: 0 Length: 3096  
Score: 4925.00 Matches: 976  
Percent Similarity: 96.9% Conservative: 14  
Best Local Similarity: 95.5% Mismatches: 32  
Query Match: 93.5% Indels: 0  
DB: 6 Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-352-179-88 (1-3096)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
DB 1 ATGGCGGAGAGCGTCTGAGCATGCGAGGTCCTGCTGGTGGGCAAGTCCCATCAGCAAGGCC 60  
QY 21 AlaSerAlaAlaAspGluThrSerLeuLeuGluGlyValGluLysAspIleTrpTyr 40  
DB 61 GCCTCTGCGCGTGGCAATAGACAGCGCTCTGCTGGCGGTGAGAGGACATCTGGTAT 120  
QY 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
DB 121 ATCAAGATGAGCTAAAGCAATATGACGCAATCTCTAGAGCTGCTGAGGTATGAAAG 180  
QY 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTrpAspIleGlu 80  
DB 181 AAAGATGAACATTAAGGTTTGGCGAGAGCAATACGTGACCTGCTGATGACATTGAA 240  
QY 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
DB 241 GATTCCTTGTAGTAATTAAGTCCATATTAAGCCAAACCTATTTCTGTCAGTTGGTG 300  
QY 101 LysLeuArgGluThrHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
DB 301 AAACCTTAGAGCGCCCGGATCGCTATCGGTATCCACCAACCTCAATCAAGAGTTGAA 360  
QY 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
DB 361 GAAGTGAGTAGAGAGACACACGCTACATTTAGTCGAGCTATTTCTCCCGGACAGAG 420  
QY 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
DB 421 GATGACATGATTCCTATGACAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA 480  
QY 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
DB 481 GCTGAGCTTGTGGGTGTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
QY 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
DB 541 GCTAATGATGCTCGGCCCAAGGTAACTGCTGCTGGGATGGTGGTTAGGCAAGACA 600  
QY 201 AlaLeuSerArgLysIlePheGluSerGluLysIleArgLysAsnPheProCysAsn 220  
DB 601 GCTCTTTTCGAGAGAGACTCTTTGAAAGCGAGAGACATAGGAGAACTTCCCTTCATT 660  
QY 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
DB 661 GCTTGGATTACAGTGTACATCATTTCCACAGGATTCAGCTACTTAAAGATATGATACGC 720  
QY 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnLeuGlnIleLysValVal 260  
DB 721 CAACCTCTTGGGCCCAAGTCTCTGATCAACTCTTGGCAAGAAATGGCAAGGAGGTGGT 780  
QY 261 ValGlnValHisIleLeuSerGluTyrLeuIleGluGluLeuLysGluLysArgTyrPhe 280  
DB 781 GTCAGATACATCACTTCTGAGTACTGTATAGAGAGCTCAAGGAGAGAGGTACTTT 840  
QY 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
DB 841 GTTATTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGCAATTT 900  
QY 301 ProLysAsnAsnLysLysGlySerArgIleValIleThrArgAsnValAspLeuAla 320  
DB 901 CCTAAGAACATTAAGAGGCGAGTGCATATGATATACCCTCGGATGTTGATCTAGCG 960  
QY 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
DB 961 GAGAAGGTGTCACAGCCCTCACTGGTGTACCACTTGTATTTCTTTCGAGATGAACGATGCC 1020  
QY 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
DB 1021 ATAACATTTGCTACTGAGAAACAAATATAATATCATGATGATGATGATGATGATGATGAT 1080

QY 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
DB 1081 ATGCAAAAGAGTGGTTGAACGAATTTGAAATAATGGTGGTCTACCATTTAGCAATACTT 1140  
QY 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHis 400  
DB 1141 ACATATGAGAGCTGTGCTTGCACACTAAACATGTGTGAGATGGAGAAATTTCTATGAACAA 1200  
QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeu 420  
DB 1201 CTTCTCTCAGAACTAGAAATAAAACCCAGCCTGGAGCTTTGAGGAGAAATGGTGACCTTA 1260  
QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
DB 1261 GGTATCAACACCATCTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGATATCTTCT 1320  
QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
DB 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGTTTGT 1380  
QY 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
DB 1381 AGACCAAGAGTTGGGATGACAGCTAGAGATGTGGAGAAAGTTACTTTAATGAGCTAATC 1440  
QY 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
DB 1441 AACCCGAGTATGATTAACGATCAAGAGTGGGATAGCAGGAAAAATTAAGACTTTGCGA 1500  
QY 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeu 520  
DB 1501 ATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAATTTTGTATTA 1560  
QY 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
DB 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACCTGCCACATAGCATTTCCAT 1620  
QY 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe 560  
DB 1621 GGGATGTATGCTCGCAAAACAGGATTTGGATGGAGCATTTATTCATCATTTAGCTATTTT 1680  
QY 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
DB 1681 GGTGACAGACCCCAAGAGTCTAGCACATGTCAGTTTGTCTAGATCAATTTAGAGATTTACGG 1740  
QY 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
DB 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTCCAGCGATTTGCA 1800  
QY 601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
DB 1801 TTGTTGTGCCACTTGAATATCTTGAATTTGGATATTTGGTTCATCATATATTCACCTTCC 1860  
QY 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
DB 1861 AGATCCATTTGGTAAACTACAGCGCTTCAAACTTTGAACATGCTGAGACATACATGCA 1920  
QY 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
DB 1921 GCACCTACCAAGTGAGATCAGTAACTCCAATGTCTGCATCTCTTCTGTTAGTAGAAG 1980  
QY 661 PheHisTyrAspAsnPheSerLysHisProMetLysCysIleThrAsnThrIleCys 680  
DB 1981 TTTGTTTATGACAACTTTTAGTCTAAACCCCAATGAAGTGCAATACTAACCAATATGC 2040  
QY 681 LeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGlu 700  
DB 2041 CTGCTTAAAGTATTTACACCTTTAGTTAGTCGCGATGATCGTGCAAAACAAATTTGCTGAA 2100  
QY 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
DB 2101 TTGCATATGGCCACCAAAAGTTGCTGGTCTGAATCATTTCCGTTGTGAAGGTACCCAAAGGA 2160



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Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSer 740
Db 2161 ATAGGTAAAGTTCGAGACTTCGAGGTTCAGAGTATGATAGATATCAGCGCGACAGTAGT 2220
Qy 741 ArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsn 760
Db 2221 AGAGCAATCAAGAGCTGGGGCACTTAAGCAAGTTGAGGAAATAGGTGTGATAACAAA 2280
Qy 761 GlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeu 780
Db 2281 GGCTCGCAAAAGAAAGAAATGTAAGATACCTTTATGAGCCATGGAAGAGCTCTCTCCCTC 2340
Qy 781 GlnSerLeuHisValAspAlaAlaGlyLysSerAspGlyGlyThrLeuGluCysLeuAsp 800
Db 2341 CAATCTCTCTATGTAATGCTGCTGTTATATCAGATATTGAACACATGAGTGCCTAGAT 2400
Qy 801 SerIleSerSerProProLeuLeuLeuArgThrLeuValLeuAspGlyLysLeuGluGlu 820
Db 2401 TCTATTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
Qy 821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLys 840
Db 2461 ATGCTTAACCTGATGAGCAGCTCACTCACTGAGAGAGATCTACTATTATTGAGGACAAA 2520
Qy 841 LeuLysGluGlyLysThrMetLeuLeuLeuLeuGlyAlaLeuProAsnLeuMetValLeuHis 860
Db 2521 CTAAGGAGAGGTAACCACTGCTGATCTGAGGAGCACTCGGGTTGAATGGAAGTCTTGAGAG 2580
Qy 861 LeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsn 880
Db 2581 CTTTATGGAATCTTACCTTGGGAGAGAGTAGTATTCAAAACGGAGGAGTCCCAAT 2640
Qy 881 LeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluLysLeuArgPheGluAspGly 900
Db 2641 CTTAGAACCTTCTGATTTTACGAATTTGATCAGCTTAAGAGAGATGAGATTGAGGATGGC 2700
Qy 901 SerSerProLeuLeuGluLysIleGluLysGlyGluCysArgLeuGluSerGlyLysThr 920
Db 2701 AGCTCACCTCTGTGGAAAGATAGAAATCTCTGCTGAGTTGGATCAGGGATATT 2760
Qy 921 GlyIleLeuHisLeuProLysLysLysGluLysLeuProLysLysLysValAla 940
Db 2761 GGTATCATTCACCTTCCCAAGGCTCAAGGAGATTTTCACTTGAATCAAAAGTAAAGTGGCT 2820
Qy 941 GlyLeuGlyGlnLeuGluGluValAlaAsnAlaHisProAsnArgProValLeuLeuMet 960
Db 2821 AGGCTTGTGCTGAGGAGAGAGTAGAACACACACACCCCAATCCCTGCTGCGAATG 2880
Qy 961 TyrSerAspArgTyrHisAspLeuGlyAlaGluLysSerSerIleGluVal 980
Db 2881 GACAGTGACCGAAGGATCACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Qy 981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000
Db 2941 CAACAGCAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Qy 1001 AspProLeuProGluGlnGluGlyLysSerGlnSerGlnValIleThrLeuThrThr 1020
Db 3001 GATCCCTCTCCGAGCAGGAGGAGAGAGCTCGAGTCCGAGTGCAGGTGATCAGTTGAGGAG 3060
Qy 1021 AsnAsp 1022
Db 3061 AACGAT 3066
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## RESULT 5

US-10-656-394A-3

; Sequence 3, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; TITLE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035718/252062

; CURRENT APPLICATION NUMBER: US/10/656,394A

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 3099

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(3099)

; US-10-656-394A-3

## Alignment Scores:

Pred. No.:	0	Length:	3099
Score:	4906.00	Matches:	971
Percent Similarity:	96.0%	Conservative:	20
Best Local Similarity:	94.1%	Mismatches:	41
Query Match:	8	Indels:	0
DB:		Gaps:	0

US-10-656-394A-8 (1-1032) x US-10-656-394A-3 (1-3099)

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Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20
Db 1 ATGGCGGAGACGGTCTGAGCATGGCGAGGTGCTGGTGGGCGAGTGCATCAGCAAGGCC 60
Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTyrTyr 40
Db 61 GCCTCTGCGCTGCCAATGAGCAGCGCTCTGCTCGCGCTCGAAGAAGGACATCTCGTAT 120
Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60
Db 121 ATCAAAGATGAGCTAAACCAATCAGGCATTCCTTAGAGCTGCTGAGTTATGAAAAAG 180
Qy 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80
Db 181 AAAGATGAACATTATAAGTTTGGCAGAGCAATACGTGACCTGCTGATGACATTGAA 240
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100
Db 241 GATTCCTCTGATGAATTTAAAGTCCATTTGAAAGCCAAACCTATTTCGTAGTTGGTG 300
Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120
Db 301 AAACCTTAGAGAGCGCCACCGGATCGCTATCCGTATCCCAACCTCAATCAAGAGTTGAA 360
Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140
Db 361 GAAGTGAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCTATTTCTCCCGCAGAG 420
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160
Db 421 GATGACATGGATTCCTATGAGAGAGACATTCGCATCAATCAGCTCGAATGTGGATGAA 480
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180
Db 481 GCTGAGCTTTGTTGGGTTTCTGACTCAAGAAGAGGCTGCTTGAATGATCGATACCAAT 540
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLysLeuGlyLysThr 200
Db 541 GCTAATGATGTCGGCCNAGTAAATCTGTGTGTTGGGATGGGTGGTTAGGCAAGACA 600
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220
Db 601 GCTCTTTTCAGGAAGATCTTTGAAGGAGGAAGACATTAGGAAGAACTTCCCTTGCAT 660
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240
Db 661 GCTTGGATTACAGTGTCAATCATTTTCAGAGGATGAGCTACTTAAGATGATGATGACG 720
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnLeuGlnGlyLysValVal 260
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QY 981 GlnThrAlaAapProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000  
Db 2941 CAAACAGCAGATCCCTGTTCCATGATGCCCAAGGATCACTGATGAGCAGTGGAAAGCAACG 3000  
QY 1001 AspProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeuThrThr 1020  
Db 3001 GATCCCTTCCGAGCAGGAGAGAGAGCTCGCAGTGCAGGTGATCAGTTGACGAGC 3060  
QY 1021 AsnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGC 3096  
RESULT 6  
US-10-656-394A-16  
; Sequence 16, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE OF INVENTION: broad-spectrum resistance gene p12  
; TITLE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656.394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq For Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 3674  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
US-10-656-394A-16

Alignment Scores:  
Pred. No.: 0 Length: 3674  
Score: 4906.00 Matches: 971  
Percent Similarity: 96.0% Conservative: 20  
Best Local Similarity: 94.1% Mismatches: 41  
Query Match: 93.1% Indels: 0  
DB: 8 Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-16 (1-3674)

QY 1 MetalGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerValAla 20  
Db 9 ATGGCGGAGACGGTCTGATGATGCGGAGGCTGCTGCTGCGGAGTGCATCAGCAAGGCC 68  
QY 21 AlaSerAlaAlaAapGluThrSerLeuLeuGlyValGluIleAspIleThrTyr 40  
Db 69 GCCTCTGCGGCTGCCAATGAGACGAGCTCTCTGCTGCGGCTCGAAGAGCATCTGGTAT 128  
QY 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIleLys 60  
Db 129 ATCAAAGATGAGTAAAAAACAATGACGAGCATCTCTGCTGCGGCTCGAAGAGCATCTGGTAT 188  
QY 61 LysAspGluLeuLeuLysValTropAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
Db 189 AAAGATGAACATTAATAAGGTTGGCGCAGCAATACGAGCTGCTGCTGATGACATGAA 248  
QY 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 249 GATTCCTTGTGATTAATTAAGTCCATATTTGAAGCCAAACCTATTTTCGTGCTGGTGTG 308  
QY 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
Db 309 AAACCTTAGAGAGCCCGGATCGCTATCCGATATCCAACTCAACCTCAATCAAGAGTTGAA 368  
QY 121 GluValSerSerArgAnthrArgTyrSerLeuValLysPheIleSerSerGlyThrGlu 140  
Db 369 GAAGTGTAGTACAGCAACACAGCTACAATTTAGTCGAGCTATTTCTCCGCGCACAGAG 428  
QY 141 IleAspMetAspSerTyrAlaGluAspIleArgGlnSerAlaArgAsnValAspGlu 160  
Db 429 GATGACATGGATTCCTATGACAGAGACATTCGCAATCAATGAGCTCGAATGTGATGAA 488

QY 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 489 GCTGAGCTTGTGGGTTTTCTGATCTCAAGAAAGGCTGCTTGAATATGATGATACCAAT 548  
QY 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 549 GCTAATGATGCTCCGCCCAAGGTAATCTGTGTTGTTGGATGGGTGGTTAGGCAAGACA 608  
QY 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 609 GCTCTTTTCGAGGAGATCTTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCCTTGGCAAT 668  
QY 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 669 GCTTGGATTTACAGTGTGCACATCTTTTCACAGANTTGAAGTACTTAAAGATATGATACGC 728  
QY 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluGlnGlyLysValVal 260  
Db 729 CAACCTTCTGGTCCCAAGTTCTCTGGAATCAACTCTTGCATGAATTCGAAGGAAAGTGGTG 788  
QY 261 ValGlnValHisIleLeuSerGluTyrLeuIleGluGluLeuLysGluLysArgTyrPhe 280  
Db 789 GTGCAAGTACATCATCTTTCTGAGTACTGATAGAAGAGCTCAAGAGAGAGGTACTTTT 848  
QY 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 849 GTTGTCTTAGATGATCTATGATGATTTTACATGATTTGGAATTTGGAATTTGCAATTT 908  
QY 301 ProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
Db 909 CCTAAGAACCAATTAAGAGGAGGAGTGCATAGTAAGAGAGCTCAAGAGAGAGGTACTTT 968  
QY 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 969 GAGAAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTCAGATGAACAGATGCC 1028  
QY 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1029 ATTTCAATGCTACTGAGAAAACAATAAATAATCATGAAGACATGGAATCAATATAAAT 1088  
QY 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1089 ATGCAAAAGATGTTGAACGAATTTGTAATAAATGTTGCTGCTACCACTTACCAATACTT 1148  
QY 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTyrGluLysPheTyrGluHis 400  
Db 1149 ACAATAGAGCTGTGCTTGCACATAAACAAGTGTGAGATGGAGAAATTTCTATGAACA 1208  
QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu 420  
Db 1209 CTTCCTTTCAAGACTAGAAAATAAACCCAGCTTGAAGCTTTTTCAGAGAAATGCTGACCTA 1268  
QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
Db 1269 GGTTCACCAACCTACATCCCATCTGAACCACTTTTGTATCTATAGTATCTTCTCT 1328  
QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1329 GAGGATTTTCAAAATACAAAGGAATCGCTTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT 1388  
QY 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
Db 1389 AGACCAAGGTTGGGATGAGCTTAGGATGTCGAGAAAGTTACTTTTATGAGCTAATC 1448  
QY 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1449 AACCGAAGTATGATTTCAACGATCAAGAGTGGGCACAGCAGCAAAAAAATAAGACTTGTGA 1508  
QY 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeu 520  
Db 1509 ATCCATGATATCATCGTGATATCATGTTTCAATCTCGACAGAGAAAAATTTTGTATTA 1568  
QY 521 LeuProMetGlyAspGlySerAspLeuValGlnGlnAsnThrArgHisIleAlaPheHis 540

Db 1569 TTACCAATGGGAGATGGCTCTGATTAGTTTACAGAAAACACATCGCCACATAGCATTTCCAT 1628  
Qy 541 GlySerMetSerCysLeuThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePhe 560  
Db 1629 GGGAGTATGTCCTGCAAAACAGGATTTGGATGGAGCATTTATTCGATCATAGCTATTTT 1688  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1689 GGTGACAGACCCAGAGCTAGCACATGCGAGTTGTTCAGATCAATTTGAGGATGTATCGG 1748  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1749 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTGCA 1808  
Qy 601 LeuLeuCysHisLeuLysThrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1809 TTGTTGTGCCACTTGAAATACCTTGAGTATTGGATATTTCGTATCCATATATTTCACTTCCC 1868  
Qy 621 ArgSerIleGlyLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1869 AGATCATTTGGTAAACTACAGGGCTTACAGCTTTGAACTTGAACTGCAAGCATACATTGCA 1928  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1929 GCACCTACCAAGTGAGATCAGTAAACTCAATGTCTGCATACTCTTCGTTGTATAAGAGAG 1988  
Qy 661 PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrLeuThrIleCys 680  
Db 1989 CTTGAATTTGCAACTTTAGTCTAAATCACCCTAAGTGAAGTCACTAATCAATATATGC 2048  
Qy 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
Db 2109 TTTTCATATGGCCACCAAAAGTTTCGGTCTGAATTCATTCGGTGTGAAGGTACCCAAAGA 2168  
Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSer 740  
Db 2169 ATAGGTAACTTGGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCATAGT 2228  
Qy 741 ArgAlaIleLysGlnLeuGlyClnLeuSerLysLeuArgLysLeuGlyValThrLeuAsn 760  
Db 2229 AGAGCAATCAAAAGCTGGGGCAGTTAAGCAAGTTGAGGAAATAGCTGTGTATCAAAA 2288  
Qy 761 GlySerThrLysGluLysCysLysIleLeuTyrAlaIleGlyLysLeuSerSerLeu 780  
Db 2289 GGCTGCACAAAGGAAATGTAAAGATCTTTATGCGCCATTCAGAGCTCTCTCCCTC 2348  
Qy 781 GlnSerLeuHisValAspAlaIleGlyLysSerAspGlyThrLeuGluCysLeuAsp 800  
Db 2349 CAATCTCTCTATATGAATCTCGGTTATTATCAGATATTTGAACACTTTGAGTGCCTAGAT 2408  
Qy 801 SerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGlu 820  
Db 2409 TCTATTTCATCT 2468  
Qy 821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLys 840  
Db 2469 ATGCTTAACCTGGATTCAGCAGCTCACTCACCTGGAAGAGTTTCAACTTATGAGTGTATAA 2528  
Qy 841 LeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHis 860  
Db 2529 CTAAGGAGGTAAAAACATGCTGTATCTTGGGCACTGCGCCACCTCATGTTCTCTCTCTCT 2588  
Qy 861 LeuTyrArgAsnAlaTyrLeuGlyLysLeuValPheLysThrGlyAlaPheProAsn 880  
Db 2589 CTTTATCATATTTCTTATCTTGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAT 2648  
Qy 881 LeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluIleArgPheGluAspGly 900

Db 2649 CTTAGAACAATTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTTGAGGACGC 2708  
Qy 901 SerSerProLeuLeuGluLysIleGluIleGlyGluCysArgLeuGluSerClyIleThr 920  
Db 2709 AGCTCACCCAGTTGGAAAAGATAGAAATCTCTTGTGCGAGTTGGAATCAGGGATTATT 2768  
Qy 921 GlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyrGlySerLysValAla 940  
Db 2769 GGTATCATCTTCCAGGCTCAAGGAGATTTCACTTTGAATACAAAAGTAAAGTGCT 2828  
Qy 941 GlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMet 960  
Db 2829 AGGCTTGGTCAAGTGAAGGAGAGTGAACACACACACCCAAATCGCCCGCTGCTGCAATG 2888  
Qy 961 TyrSerAspArgAspTyrHisAspLeuGlyValAlaGluGlySerSerIleGluVal 980  
Db 2889 GACAGTGACCAAGGATCAGACCTGGGGCTGAAGCCGAGGATCTTCTATAGAGTG 2948  
Qy 981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000  
Db 2949 CAAACAGCAGATCTCTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAAG 3008  
Qy 1001 AspProLeuProGluGlnGlyGlyGlySerSerGlnSerGlnValIleThrLeuThr 1020  
Db 3009 GATCCCTTCCCGAGCAGAGGAGAGAGCTCGCAGTCCGAGGTGATCAGTTGACGAG 3068  
Qy 1021 AsnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3069 AATGATAGCAAGAGATAGGACACAGCTCAAGCTGGC 3104

## RESULT 7

US-10-352-179-83

; Sequence 83, Application US/10352179

; Publication NO. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl

; FILE REFERENCE: 2727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; PRIOR FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 83

; LENGTH: 76272

; TYPE: DNA

; ORGANISM: Oryza minuta

US-10-352-179-83

Alignment Scores:

Pred. No.:	0	Length:	76272
Score:	4753.00	Matches:	938
Percent Similarity:	96.8%	Conservative:	14
Best Local Similarity:	95.4%	Mismatches:	31
Query Match:	90.2%	Indels:	0
DB:	6	Gaps:	0

US-10-656-394A-8 (1-1032) x US-10-352-179-83 (1-76272)

Qy 40 TyrIleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaIleGluLeuMetLys 59  
Db 62063 TATATCAAGATGAGCTAAACCAACGATGCAAGCATCTCTTAGCTGCTGAACCTTATGAAA 62122  
Qy 60 LysLysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIle 79  
Db 62123 AAGAAAGATGAATTAAGGTTGGCAGAGCAATACGTACCTGTCTATATGACATT 62182  
Qy 80 GluAspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeu 99  
Db 62183 GAAGATTCCCTTGATGAATTTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTGAGTTG 62242

Qy 100 ValLysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgVal 119  
Db 62243 GTGAAATCAGAGAACGCCCAAGTTCATTCGGTATCCACACCTTAATAACAGAGTT 62302  
Qy 120 GluGluValSerSerArgAsnThrArgTyrSerLeuValLysProLysSerGlyThr 139  
Db 62303 GAAGAGTGTAGTAGGAGAACACACGCTACAGTTTGTAGTCAAGCCATTTCTCTGGCACA 62362  
Qy 140 GluIleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159  
Db 62363 GAGATTGACATGGATTCTTATCGAAGACATTCGTAAATCAGTCAGTCGCAATGGAT 62422  
Qy 160 GluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThr 179  
Db 62423 GAAGCTGAGCTTGTGGTCTTCTGACTCCAAGAAAGGTTGCTTGAATGATCGATACC 62482  
Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLeuGlyLys 199  
Db 62483 AATGCTTAATGATGTGTCGGCCAAAGTAATCTGTGTGTGGATGGGTGGTTAGGCAAG 62542  
Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219  
Db 62543 ACAGCTCTTTCAGGGAAGATCTTTGAAGCGAAGACATAGGAAGACTTCCCTTGC 62602  
Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239  
Db 62603 AATGCTTGGATTACAGTGTCAATCATTTACAGGATGAGCTACTCAAGATATGATA 62662  
Qy 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGlyLysVal 259  
Db 62663 CGCCAACTCTAGTCCCAATCTCTGAAACACTCTTCAGNAATGCAAGGAAGGTG 62722  
Qy 260 ValValGlnValHisIleLeuSerGluTyrIleLeuGluLeuLysGluLysArgTyr 279  
Db 62723 GTGGTCAAGTATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTAC 62782  
Qy 280 PheValValLeuAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299  
Db 62783 TTTGTATTCTAGATGATCTAGTATTTTACATGATGGAATGGATTAATGAAATGGCA 62842  
Qy 300 PheProLysAsnAsnLysGlySerArgIleValIleThrArgAsnValAspIle 319  
Db 62843 TTTTCTTAAGAACAAATAAGAGGCGAGTCGAATAGTAATAACCTCGAATGTGTATCTA 62902  
Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAsp 339  
Db 62903 GCGGAGAGTGTGCCAGCTCCTACTGGTGTACCACTTGATTTCTTCAGATGAACGAT 62962  
Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
Db 62963 GCCATTAACATTTGCTACTAGAAACAAATAAATCATGAAGACATGGAATCAATATAA 63022  
Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
Db 63023 AATATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGTCTACCATTAGCAATA 63082  
Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGlu 399  
Db 63083 CTTACAAATAGGAGCTGTGCTGCAACTAAACATGTGTGAGAAATGGAATAATCTATGAA 63142  
Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThr 419  
Db 63143 CAGCTTCTCTAGACTAGAAATAAACCAAGCTTGAAGCTTTGAGGAGATGGTGACC 63202  
Qy 420 LeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhe 439  
Db 63203 CTAGGTTACACCACTACCTCCATCTGAAACCATGCTTTTGTATCTAGATATCTTT 63262  
Qy 440 ProGluAspPheGluIleArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
Db 63263 CCTGAGATTTTGAATCAAAAGGAATCTCTGTGTAGTGTAGATAGATAGCAAGGGTTT 63322  
Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeu 479

Db 63323 GTTAGACCGAGTTGGGATGACGACTAAGATGTCGAGAAAGTTACTTTAATAGCTA 63382  
Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
Db 63383 ATCAGCGGAGTATGATTCAACGATCAAGAGTGGCATAACGAGAAATTAAGACTGT 63442  
Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
Db 63443 CGAATCCATGATATCATCCGATATCACAGTTTCAATCTCGAGACGAGAAATTTGTA 63502  
Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
Db 63503 TTGTTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAACACTGCCACATAGCATTC 63562  
Qy 540 HisGlySerMetSerCysLeuThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
Db 63563 CATGGAGTATGTCCTGCAAAACAGGATGGATTTGGAGCATTAATTCATATTAGCTATT 63622  
Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
Db 63623 TTTGTGTACAGACCCCAACGAGTCTAGCACATGTCAGTTTGTCTAGATCAATTTGAGGATGTTA 63682  
Qy 580 ArgValLeuAspLeuLysValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
Db 63683 CGGGTCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATT 63742  
Qy 600 AlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeu 619  
Db 63743 GCATTTGTTGCGCACTTGAATACTTCAGTATTGGATATTCGTCATCATATATTACATT 63802  
Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIle 639  
Db 63803 CCCAGATCCATTTGGTAAACTACAGGGCTTCAAACTTTGAACATGCTGAGAACATACATT 63862  
Qy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659  
Db 63863 GCAGCACTACCAAGTGAGATCAGTAAACTCCAATGCTGCATATCTCTGTTGTAGTAGA 63922  
Qy 660 GlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 63923 AAGTTGTTTATGACACTTTAGTCTAAACCCCAATGAAGTGAATTAACCAATTA 63982  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAla 699  
Db 63983 TGCCTGCCTAAAGTATTACACCTTTAGTTAGTTCGCGATGATCGTGCNAACAAATGCT 64042  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 64043 GAATTGCAATGGCCACCMAAGTTGCTGTCTGAATCATTCGGTGTGAAGGTACCCTAA 64102  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArgThrSer 739  
Db 64103 GGAATAGGTAAAGTTCGAGACTTCAGGTTCTAGATATGTAGATATCAGCGGACCACT 64162  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThr 759  
Db 64163 AGTAGAGCAATCAAGAGCTGGGGCACTTAAGCAAGTTGAGGAATTTAGGTGTGATAACA 64222  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSer 779  
Db 64223 AAAGCTCGACAAAGGAAATATAGATATCTTTATGACGCCATTGAGAGGCTCTCTCC 64282  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799  
Db 64283 CTCCAATCTCTATGTGAATGCTGCGTTATTTATCAGATATTGAAACACTTTGAGTGCCTA 64342  
Qy 800 AspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 819  
Db 64343 GATTCATTTCTATCT 64402  
Qy 820 GluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSer 839

Db 64403 GAGATGCCCTAACTGATGACGACCTCACTCACTGAGAGAGATCTACTATTGAGGAGC 64462  
Qy 840 LysLeuLysGluGlyLysThrMetLeuLeuLeuGlyAlaLeuProhenLeuMetValLeu 859  
Db 64463 AAACTAAAGGAAGGTAACCATCTGATCTTGGGGCATTTGCCCAACCTCATGTGCTTT 64522  
Qy 860 HisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPhePro 879  
Db 64523 TAATCTTAATGGAATGCTTACTTGGGAGAGAGCTAGTATTCAAACGGGAGCATTCCTCA 64582  
Qy 880 AsnLeuArgThrLeuTyrPileTyrGluLeuAspGlnLeuArgGluLeuPheGluAsp 899  
Db 64583 AATCTTAGAACAATCTGATTTAGCAATTCAGATCAGCTAAGAGAGATGAGATTGAGGAT 64642  
Qy 900 GlySerSerProLeuLeuLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 919  
Db 64643 GGCAGCTACCCCTGTTGGAAAGATAGAAATCTCTTGGTGCAGGTTGGATCAGGGATT 64702  
Qy 920 ThrGlyIleLeuHisLeuProLysLeuLysGluLeuProIleArgTyrGlySerLysVal 939  
Db 64703 ATTGGTATCAATTCACCTTCCCAAGCTCAAGGAGATTCTACTGGAATACAAAGTAAGTG 64762  
Qy 940 AlaGlyLeuGlyGlnLeuGlyGluValAsnAlaHisProAsnArgProValLeuLeu 959  
Db 64763 GCTAGGCTTGGTCACTGGAGGAGAGAGTGAACACACCCCAATCGCCCGTGTGCGA 64822  
Qy 960 MetTyrSerAspArgTyrHisAspLeuGlyAlaGluLeuGlySerSerIleGlu 979  
Db 64823 ATGGACAGTGACCGAAGGATCACGACCTGGGGGTGACCGAGGATCTTCTATAGAA 64882  
Qy 980 ValGlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAla 999  
Db 64883 GTGCAACACGACGATCTCTGTCCTGATGCGGAGAGATCAGTCACTGTAGCAGTGAAGCA 64942  
Qy 1000 ThrAspProLeuProGluGlnGluGlySerSerGlnSerGlnValIleThrLeuThr 1019  
Db 64943 ACGGATCCCTTCCCGACGAGGAGGAGAGAGCTCGCAGTGCAGGTGATCAGTTGAGC 65002  
Qy 1020 ThrAsnAsp 1022  
Db 65003 ACGAACGAT 65011

## RESULT 8

US-10-437-963-37316  
; Sequence 37316, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 37316  
; LENGTH: 4596  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_41056C.1  
US-10-437-963-37316

## Alignment Scores:

Pred. No.: 0 Length: 4596  
Score: 4397.50 Matches: 862  
Percent Similarity: 97.3% Conservative: 11

Best Local Similarity: 96.1% Mismatches: 17  
Query Match: 83.5% Indels: 7  
DB: 7 Gaps: 3

US-10-656-394A-8 (1-1032) x US-10-437-963-37316 (1-4596)

Qy .135 IleSerSerGlyThrGlu-----IleAspMetAspSerTyrAlaGluAspIleArgAsn 152  
Db 4 GTGGCACTGGCAACCACTGCTTACCAATAGATTCCTATGCAGAAAGACATTCGCAAT 63  
Qy 153 GlnSerAlaArgAsnValAspGluAlaGluLeuValGlyPheSerAspSerLysLysArg 172  
Db 64 CAATCAGCTCGAAATGTGGATGAAGCTGAGCTTGTGGGTTTTCTGACTCCAAAGAAAGG 123  
Qy 173 LeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysValIleCysValVal 192  
Db 124 CTGCTTGAATGATCGATACCAATGATGATGTCGGCCCAAGATTAATCTGTGTGTT 183  
Qy 193 GlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGluGluAsp 212  
Db 184 GGGATGGGTGGTTTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTGAAGCGAAGAAC 243  
Qy 213 IleArgLysAsnPheProCysAsnAlaTyrIleThrValSerGlnSerPheHisArgIle 232  
Db 244 ATTAGGAAGAACTTCCCTTCCCAATGTTGGATTCAGTGTCAATCATTTTCAAGGATT 303  
Qy 233 GluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeu 252  
Db 304 GAGCTACTTAAAGATATGATACGCCAACTTCTTGGCCCGCAGTTCTCTGGATCAACTCT 363  
Qy 253 GlnGluLeuGlnGlyLysValValGlnValHisLeuSerGluTyrLeuIleGlu 272  
Db 364 CAAGAATTGCAGGAGAGAGTGGTGGTGAAGTACATCATCTTCTGAGTACTGATAGAA 423  
Qy 273 GluLeuLysGluLysArgTyrPheValValLeuAspAspLeuTyrPileLeuHisAspTrp 292  
Db 424 GAGCTCAAGGAGAGAGGATCTTGTGTTTCTAGATGATCTATGGAATTTTACATGATTGG 483  
Qy 293 AsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleValIle 312  
Db 484 AATTGGATAAATGAATTTGCAATTTCTTAGAACAAATAGAGGGCAGTCAATAGTAGTAATA 543  
Qy 313 ThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValThrHisLeu 332  
Db 544 ACCACTCGGAATGTTGATCTTGGGAGAGAGTGGCCACAGCTCACTGGTGTACCCACTT 603  
Qy 333 AspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHis 352  
Db 604 GATTTCTTGCAGATGAACGATGCCATACATTTGCTACTGAGAAACCAATATAAATCAT 663  
Qy 353 GluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLysCys 372  
Db 664 GAAGACATGGATCAATAAATAATATGCAAAAGATGTTGAACGAATTTGTAATAAATGT 723  
Qy 373 GlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnValSer 392  
Db 724 GGTGCTCTACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCACCTAAACAGGTGCA 783  
Qy 393 GluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsnProSerLeuGlu 412  
Db 784 GAATGGGAGAAATTTCTATGAACACCTTCTTCAAGAACTAGAAATAAACCCAGCCCTGAA 843  
Qy 413 AlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCys 432  
Db 844 GCTTTGAGGAGAAATGGTGACCTTAGGTATCAACACCATCTACCATCCCTCTGAAACCATGC 903  
Qy 433 PheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGly 452  
Db 904 TTTTGTATCTAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGT 963  
Qy 453 ArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGly 472  
Db 964 AGATGGATAGCAGAAAGGTTTGTAGACCAAAAGGTTGGGATGACGACTAAAGATGTGCGA 1023

473 GluSerTyrPheAsnGluLeuLeuAsnArgSerMetIleGlnArgSerArgValGlyIle 492  
Db 1024 GAAAGTTACTTTAAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATA 1083  
Qy 493 AlaGlyValIleValThrCysArgIleHisAspIleIleArgAspIleThrValSerIle 512  
Db 1084 GCAGGMAAATTAAGACTTGTGCAATTCATGATATCATCCGATATCAAGTTCAATC 1143  
Qy 513 SerArgGlnGluAspPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGlu 532  
Db 1144 TCAGACAGAGAAATTTTGTATTTGTTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAA 1203  
Qy 533 AsnThrArgHisIleAlaPheHisGlySerMetSerCysIleThrGlyLeuAspTrpSer 552  
Db 1204 AACCTCGCCCATAGCAATTCATGGGAGTATGCTCGCAAAACAGANTTGGATGGAGC 1263  
Qy 553 IleIleArgSerLeuAlaIlePheGlyAspArgProIleSerLeuAlaHisAlaValCys 572  
Db 1264 ATTATTCGATCATTTAGCTATTTTGTGTCAGACAGCCCAAGAGTCTAGCACATCGAGTTGT 1323  
Qy 573 ProAspGlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeuIleThr 592  
Db 1324 CAGATCAATTCAGGATGTTACGGGTCTTGGATCTTGAAGTGTGACATCTTAAATCACT 1383  
Qy 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612  
Db 1384 CAAAGAGATTCGACCATATTTGTCATTTGTTGGCCACTTGAATATCTTGAGTATTCGATAT 1443  
Qy 613 SerSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeu 632  
Db 1444 TCGTCATCATATATTCCTTCCAGATCCATTTGGTAAACTACAGGGCCCTACAAATCTTG 1503  
Qy 633 AsnMetProSerThrTyrIleAlaLeuProSerGluIleSerLysLeuGlnCysLeu 652  
Db 1504 AACATGCCGAGCACATACATTCGACGACTACCAAGTGAGATCAGTAAATCTCCAAATGTCTG 1563  
Qy 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672  
Db 1564 CATACTCTTCGTTGTATAGGACAGTTTCATATGACAACTTTAGTCTAAACCCCAATG 1623  
Qy 673 LysCysIleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAsp 692  
Db 1624 AAGTGCATAACTAACACAAATATGCTGCTAAAGTATTCACACTTTAGTTAGTCGCAT 1683  
Qy 693 AspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSer 712  
Db 1684 GATCGTGCAAAACAAATTTGCTGAATTCACATGGCCACCAAAATGCTGGTCTGAATCA 1743  
Qy 713 IleGlyValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyr 732  
Db 1744 TTCGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTAT 1803  
Qy 733 ValAspIleArgThrSerSerArgAlaIleIleGlyLeuLeuGlyLeuSerLysLeu 752  
Db 1804 GTAGATATCAGCGGACCAAGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTG 1863  
Qy 753 ArgLysLeuGlyValThrAsnGlySerThrLysGlyLysCysLysIleLeuTyrAla 772  
Db 1864 AGGAATTAGTGTGCACAAACAAACGGGTGACAAAGGAAATGTAAGTACTTTATGCA 1923  
Qy 773 AlaIleGlyLysLeuSerSerLeuGlnSerLeuHisValAspAla-----AlaGly 789  
Db 1924 GCCATTTGAAGACTCTCTTCCCTCCAATCTCTCCATGTGGATGCTGTGTATTCTTCAGGT 1983  
Qy 790 IleSerAspGlyGlyThrLeuGluCysLeuAspSerIleSerProProLeuLeu 809  
Db 1984 ATTATT-----GGAAACACTTGAAGTCTAGATTTCTATTCATCTCTCTCTCTACTA 2037  
Qy 810 ArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrpIleGluGlnThr 829  
Db 2038 AGGACACTCAGGTTGAATGGAAGTCTTTGAAGAGATGCTTAACCTGGATTCAGAGCTCACT 2097

Qy 830 HisLeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyThrMetLeuIle 849  
Db 2098 CACCTTGAGAGAGTTTCGACTTTACGGAGAGTAACTAAAGGAGGTAAACACCTGCTGATA 2157  
Qy 850 LeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGlu 869  
Db 2158 CTTGGGCGATTTGCCAACCTCATGTCCTTATCTTATCGGAATGCTTACCTTTGGGAG 2217  
Qy 870 LysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeu 889  
Db 2218 AAGCTAGTATTTCACAAACGGGAGCATTTCCCAAAATCTTAGAACACTTTGTTATTACGAATTG 2277  
Qy 890 AspGlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGlu 909  
Db 2278 GATCAGCTAGAGAGATCAGATTTTGAAGGAGCGGAGCTCACCTCTTGGAAAAGATAGAA 2337  
Qy 910 IleGlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLys 929  
Db 2338 ATAGGCAAGTCGAGGTTTGGAAATCTGGGATTTATTTGGTATCATTTACCTTTCCAAAGCTCAAG 2397  
Qy 930 GluIleProIleArgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyGluVal 949  
Db 2398 GAGATTCATATACATACGAGAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGAGAGTG 2457  
Qy 950 AsnAlaHisProAsnArgProValLeuLeuMetTyrSerAspArgTyrHisAspLeu 969  
Db 2458 AACACACACCAAAATCGCCCGTGTGCTTAATGTACAGTGACCGAAGGTATCACGACCTG 2517  
Qy 970 GlyValGluAlaGluGlySerSerIleGlyValGlnThrAlaAspProValProAspAla 989  
Db 2518 GGGGCTGAGCCGAGAGATCTTCTATAGAACTGCAACAGCAGATCTCTGTTCTCTGATGCC 2577  
Qy 990 GluGlySerValThrValAlaValGluAlaThrAspProLeuProGluGlnGlyGlu 1009  
Db 2578 GAAGGATCAGTCACTGTAGCAGTGGAGCAACGAGTCCCTTCCCGAGCAGGAGGAGAG 2637  
Qy 1010 SerSerGlnSerGlnValIleThrLeuThrThrAsnAspSerGluGluIle 1026  
Db 2638 AGCTCGCAGTCGCGAGGTGATCAGTTGACAGCAATGATAGAAATCGTCTTA 2688

## RESULT 9

US-10-656-394A-11  
; Sequence 11, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11:  
; LENGTH: 2997  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)....(2997)  
US-10-656-394A-11

Alignment Scores:  
Pred. No.: 0 Length: 2997  
Score: 4241.50 Matches: 861  
Percent Similarity: 84.8% Conservative: 17  
Best Local Similarity: 83.2% Mismatches: 49  
Query Match: 80.5% Indels: 108  
DB: 8 Gaps: 5

US-10-656-394A-8 (1-1032) x US-10-656-394A-11 (1-2997)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20

|||||  
1 ATGGCGGAGACGGTGTGAGCATGGCGAGGTCTGGTGGGAGCGCCATCAGCAAGGCC 60  
21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTyr 40  
61 GCCTCGCGCGTGGCGAGACAGCCCTCTCTGCTGGCGTGGAGAGACATCTGGTAC 120  
41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
120 ----- 120  
61 LysAspGluLeuLysValTrrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
120 ----- 120  
81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
121 -----TTGTTTAGACATGGTGT 138  
101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
138 ----- 138  
121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
139 -----GGACGGTCCGAATGGTGGGCTGTGTTAGGTATGGTGGCATCTGGCAACCG 189  
141 -----IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnVal 158  
190 TCATGCTTAGCAATAGATTCCTATGCAGAGACATCCCAATCAATCAGCTCGAATGTG 249  
159 AspGluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAsp 178  
250 GATGAAGCTGAGCTGTGTTGGGTTTCTGACTCCCAAGAAAGCGTCTGGAATGATCGAT 309  
179 ThrAsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGly 198  
310 ACCAATGCTTAATGATGGTCCGCGCAAGGTAATCTGTGTGTTGGATGGGTGTAGGC 369  
199 LysThrAlaLeuSerArgLysIlePheGluSerGluLeuAspIleArgLysAsnPhePro 218  
370 AAGACAGCTCTTTCCAGGAAGATCTTTGAAAGCGAAGACAGACATAGGAAGAACTTCCT 429  
219 CysAsnAlaTrrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMet 238  
430 TGCAATGCTTGGATTACAGTGTCACAATCTTACAGGATGAGCTACTTAAAGATAG 489  
239 IleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnIleGlyLys 258  
490 ATACGCCAATCTTGGCCCCAGTTCTCTGGATCACTCTTGCAAGAAATGGCAAGGAAG 549  
259 ValValValGlnValHisIleSerGluTrrpLeuIleGluLeuLysGluLysArg 278  
550 GTGGTGGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGG 609  
279 TyrPheValValLeuAspLeuTrrpIleLeuHisAspTrrpAsnTrrpIleAsnGluIle 298  
610 TACTTTGTTGTTAGATGATCTATGGATTTTACATGATTGGAATGGATAAATGAAT 669  
299 AlaPheProLysAsnLysLysGlySerArgIleValIleThrThrArgAsnValAsp 318  
670 GCATTTCTTAAGAACAAATAGAGGCGAGTCAAAATAGTAATAACCACTTGGAAATGTGAT 729  
319 LeuAlaGluLysCysAlaThrAlaSerLeuValTrrpHisIleAspPheLeuGlnMetAsn 338  
730 CTTGGCGGAGAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTGTGCAGATGAAC 789  
339 AspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsn 358  
790 GATGCCATACATTTGCTACTGAGAAAAAATAAATAAATCAATGATGAAGCATGGAAATCAAT 849  
359 LysAsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAla 378  
|||||

850 AAAAATATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTGGTCTACCATTAGCA 909  
379 IleLeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrrpGluLysPheTyr 398  
910 ATACTTAAATAGAGCTGTGCTTGAACATAACAGGTGTGAGATGGAGAAATCTTAT 969  
399 GluHisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetVal 418  
970 GAACACCTTCTTCCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGAAATGGTG 1029  
419 ThrLeuGlyTrrpAsnHisLeuProSerHisLeuLysProCysPheLeuTrrpLeuSerIle 438  
1030 ACCCTAGGTATCAACCAACCTACCATCCATCTGAAACCAATGCTTTTGTATCTAAGTATC 1089  
439 PheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrrpIleAlaGluGly 458  
1090 TTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGTAGTGCAGAGAGG 1149  
459 PheValArgProLysValGlyMetThrThrLysAspValGlyGluSerTrrpPheAsnGlu 478  
1150 TTTGTTAGACCAAAAGGTGGGATGACGACTAAGGATGTGCGAGAAAGTTACTTTAATGAG 1209  
479 LeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThr 498  
1210 CTATATCAACCGAAGTATGATTTCAACGATCAAGAGTGGCATAGCAGGAAAAAATTAAGACT 1269  
499 CysArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPhe 518  
1270 TGTGCAATTTATGATATCATCCGTGATATCACAGTTTCAATCTCGAGAGACAGAAAAATTTT 1329  
519 ValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAla 538  
1330 GTATTTGTTACCAATGGAGATGGCTCTGATTTAGTTTCAGAAAAACACTGCCACATAGCA 1389  
539 PheHisGlySerMetSerCysLysThrGlyLeuAspTrrpSerIleIleArgSerLeuAla 558  
1390 TTCCATGGGAGTATGTCCTGCAAAACAGGATTTGGATTGGAGCATTTATTCGATCATAGCT 1449  
559 IlePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMet 578  
1450 ATTTTGTGTGACACACCAAGAGCTTAGCACATGTCAGTTTGTTCAGATCAATTTGAGGATG 1509  
579 LeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArg 598  
1510 TTACGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGT 1569  
599 IleAlaLeuLeuCysHisLeuLysTrrpLeuSerIleGlyTrrpSerSerIleTrrpSer 618  
1570 ATTTGATTTGTTGTCCTTGAATACTTGAATACTTGAATACTTGAATACTTGAATACTTGA 1629  
619 LeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyr 638  
1630 CTTCCAGATCCATTTGGTAAACTACAGGGCTTACAAACTTTGAACTGCGAGCAGCATAC 1689  
639 IleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIle 658  
1690 ATTTGACGACATACCAAGTGAGTCACTTGAATACTTGAATACTTGAATACTTGAATACTTGA 1749  
659 GlyGlnPheHisTrrpAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThr 678  
1750 AGAAATTTGTTTCTGCAACTTTTAGTCTTAAACCAACCACTTAAAGTGAATCAATAACACA 1809  
679 IleCysLeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIle 698  
1810 ATATGCTGCTTAAAGTATTCACACCTTTAGTTAGTGGATGATCGTGCATATCAAAAT 1869  
699 AlaGluLeuHisMetAlaThrLysSerCysTrrpSerGluSerIleGlyValLysValPro 718  
1870 GCTGATTTGCATATGGCCACCAAAAGTTGCTGGTATAAATCATTTTCGTTGAGGTACCC 1929  
719 LysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTrrpValAspIleArgThr 738  
1930 AAAGGAATAGGTAAAGTTCGAGACTTACAGGTTCTTAGAGTATGTAGATATCAGGCGGACC 1989



Qy 739 SerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThr 758  
Db 1990 AGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAAGCAAGCTGAGGAATATAGGTGTGATG 2049  
Qy 759 ThrAsnGlySerThrLysGluLysCysLysValLeuTyrAlaAlaIleGluLysLeuSer 778  
Db 2050 ACAATGGCTGCACAAAGGAAATGTAAGTACTTTGTGCGAGCCATTGGAAGCTCTCT 2109  
Qy 779 SerLeuGlnSerLeuHisValAspAlaAlaGlyLysSerAspGlyThrLeuGluCys 798  
Db 2110 TCCCTCCAAATATCTCTATGAATGCTGCAGGAATCTCAGATGTGGAACACTTGAAGTGC 2169  
Qy 799 LeuAspSerLysSerProProLeuLeuArgThrLeuValLeuAspGlyLysLeu 818  
Db 2170 CTAGATCTTATTTCT 2229  
Qy 819 GluGluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysLysLysLeuArg 838  
Db 2230 GAAGAGATGCTAACTGGATTGAGCAGCTCACTCACTGGAAGAGATCTACTTATTGAGG 2289  
Qy 839 SerLysLeuLysGluLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetVal 858  
Db 2290 AGCAACTAAAGAGAGTAACCACTGCTGATCTTGGGGCATTGCCAACCTCATGCTC 2349  
Qy 859 LeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPhe 878  
Db 2350 CTTGATCTTTATCGGAAAGCTTACCTTGGGGAGAGCTAGTATTCAAAAACAGAGCATTC 2409  
Qy 879 ProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluIleArgPheGlu 898  
Db 2410 CCAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTAGATTGAG 2469  
Qy 899 AspGlySerProLeuLeuGluLysLysLysLysLysLysLysLysLysLysLys 918  
Db 2470 GACGGCAGCTCGCCCGAGTTGGAAGAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGG 2529  
Qy 919 IleThrGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 938  
Db 2530 ATTATTTGGTATTATCCACCTTCCAAAGCTCAAGGAGATTTCATCTGGATACGAAGTAA 2589  
Qy 939 ValAlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeu 958  
Db 2590 GTGGCTGGCTGTCTCAGCTGAGGAGAGAGTGGCCACACACCAAAATCACCCTGCTGTG 2649  
Qy 959 LeuMetTyrSerAspArgTyrHisAspLeuGlyAlaGluAlaGlySerSerLys 978  
Db 2650 CGAAGAGGAGGAGGAGGAGGATCAGCACCTTCTGTCGACCCGAGAGATCCCTGTT 2709  
Qy 979 GluValGlnThrAlaAspProValProAspAlaGlySerValThrValAlaValGlu 998  
Db 2710 GAA-----GTGGAA 2718  
Qy 999 AlaThrAspProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeu 1018  
Db 2719 GCAACGGATCCCTCCAGAGCAGGAGGAGAGAGC----- 2754  
Qy 1019 ThrThrAsnAsp-SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 2755 -----TCGACGGAAGAGATAAGCACAGCTCAAGCTGGT 2788

## RESULT 10

US-10-437-963-2483  
; Sequence 2483, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 2483  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102251C.1  
; US-10-437-963-2483

Alignment Scores:  
Pred. No.: 0 Length: 2982  
Score: 3664.50 Matches: 733  
Percent Similarity: 81.6% Conservative: 76  
Best Local Similarity: 73.9% Mismatches: 122  
Query Match: 69.6% Indels: 61  
DB: 7 Gaps: 2

US-10-656-394A-8 (1-1032) x US-10-437-963-2483 (1-2982)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 178 ATGGCGGAGAGCGGTGCTGAGCATGGCGAGTCTGCTGGCGAGTGCCTATCAGCAAGGCC 237  
Qy 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTrpTyr 40  
Db 238 ACCTCTGCGCGCGGCCATGAGGCGAGCTCTACTCGGCGTCCAGAGGACATCTGGTAT 297  
Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
Db 298 ATCAAAGATGAGTGTAAAGGTTTGGCGAGACATGAGTACGTGCTGCTTATGAAGAAG 357  
Qy 61 LysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
Db 358 AAAGATGAGTCTTTAAAGGTTTGGCGAGACATGAGTACGTGCTGCTTATGAAGAAG 417  
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 418 GATTGCTTGCAGCAATTCAGGTCATATTTAGAGGCCAAATCTGTTTATCAGATGCTG 477  
Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
Db 478 AAGCTCAGAAAGCGCCATCTGATAGTACCCAAATCCGTAACCTCAAATCAAGAGTTGAA 537  
Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
Db 538 GAAGTGAGTAGCAGAAACTCAGCTACAAATTTAGTCAAACTATTTCATCCAGCAATGAG 597  
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
Db 598 GATGACATGGATCTTACGAGAGGACATTCGTAATCAGTCACTCACTAGCAATGTAGATGAA 657  
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuGluMetIleAspThrAsn 180  
Db 658 ACTGAGCTTGTGGGGTTCTCTGACTCTAAG----- 687  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLeuGlyLysThr 200  
Db 687 ----- 687  
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 687 ----- 687  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIleArg 240  
Db 688 -----ATAAGATTGAGCTACTACTCAAGATATGATACGG 720



QY 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnLeuGlnLeuValVal 260  
DB 721 CAATTTCTAGGTTCCAAATTCAGTCAAGTTCGAGAATTCGAGGGAAAAATGGT 780  
QY 261 ValGlnValHisLeuSerGluTyrLeuLeuGlnLeuLeuGlnLeuValPhe 280  
DB 781 GTGCAAAATACCTCATCTTCGACTCTTCGAGAAAAGCTTCAGGAAAAGAGGTATTTT 840  
QY 281 ValValLeuAspAspLeuTrrPileLeuHisAspTrrPileAsnGluLeuAlaPhe 300  
DB 841 GTTGTCTTGGATCTATGCTCTTAGATGTCATGAACTGGATTAATGATATTCATTT 900  
QY 301 ProLysAsnAsnLysGlySerArgIleValIleThrThArgAsnValAspLeuAla 320  
DB 901 CCTAAGATAACAATAAGGGCAGTCGGAATGTAGTAAACACAGAGATGTGGTCTAGCC 960  
QY 321 GlnLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
DB 961 GAGAGGTGTACCACAACTTCCTTAGTCTACCATCTTGAAACACTTGCAGATGAATGATGCC 1020  
QY 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
DB 1021 ATAACCTTGTCTAGTACGAGAAAACAAATAGAACACATGAGGACATGGGAAACAAACAAAT 1080  
QY 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
DB 1081 ATGCAAAATAATAGTTGAACAAATTTGAATAAGTGTGGCGCTACCATTTAGCGATCTT 1140  
QY 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrrPileGlnLysPheTrrGluHis 400  
DB 1141 ACAATAGGAGCTGTGTGGCAACTAAACAAAGTTTTAGATGGGAGAAATTTTTATAACAG 1200  
QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeu 420  
DB 1201 CTTCTCTCAGAACTTGAAGCAACCCAGGCTTCAAGCTTTGAGAGATGTGACCCCTT 1260  
QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTrrLeuSerIlePhePro 440  
DB 1261 GGCTACCAACCTGCCATCTCATCTGAAATCATGCTTTTGTACCTAAGATATCTTCCT 1320  
QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrrPileAlaGluGlyPheVal 460  
DB 1321 GAGGATTTGAGATCAAAAGAGTGCCTTGGTAGACAGATGGATTCAGAGGGGTGTGT 1380  
QY 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
DB 1381 AGAGCCAAAGTTGGGATGACGACGAGGATGTGGGGACAGATTACTTTAATGAGCTAATC 1440  
QY 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
DB 1441 AACCGAAGTATGATTCAAAGATCAAGAGTGGGCATAGAGGAAAATTAAGAGTGGCGA 1500  
QY 501 IleHisAspIleLysArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
DB 1501 GTCCATGATATCATGCGTGATACAGTTTCAATCTCTAGAGGAGAGAACTTTGTATTC 1560  
QY 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
DB 1561 TTACCAAGTGCATGTGGCTCCAAATCTAGCACAGGAAAACACTGCCACATAGCATGTGCAT 1620  
QY 541 GlySerMetSerCysLysThrGlyLeuAspTrrPileLysIleArgSerLeuAlaIlePhe 560  
DB 1621 GGGAGCATGTCTGCAAAACAGGATTTGGATTTGGAGCATTTATTCATCTTAGCTATTTT 1680  
QY 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
DB 1681 GGTGACAGACCCAAATAATCTAGCACACATATTTGTTCAATAAATTCAGGATTTAGCG 1740  
QY 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
DB 1741 GTCTTGGATCTTGAAGATGTGAAGTTTTTAATCACACAAAAAGATTTCAACATATAGCA 1800  
QY 601 LeuLeuCysHisLeuLysTyrLeuSerIleGly-----TyrSerSerSerIleTyrSer 618

DB 1801 TTGTTCGTTCACCTTGAAGTACTTGAAGTTCCTGAGAAATATTTCTCATCATGATATATCT 1860  
QY 619 LeuProArgSerIleGlyLysLeuGlnGlnLeuGlnThrLeuAsnMetProSerThrTyr 638  
DB 1861 CTTCCAGATCTATTTGGTAAATTTACATGCTTACAGACCTTGAATATGTCAAGTACATAC 1920  
QY 639 IleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisLeuLeuArgCysIle 658  
DB 1921 ATTGCAACACTACCACTAGATAGATCACTAACTCCAAATGTCTGCGCACTCTTCTGTGTACA 1980  
QY 659 GlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThr 678  
DB 1981 AGGGTATCTTAATAAACAATTTTAGTATAAATCAACCCGTTGAAGTCTTAACAAACA 2040  
QY 679 IleCysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaGlnIle 698  
DB 2041 ATGTGTCTGCTTAATATATTTACACCTTCAGTTAGTACGACATCTGTCGCCAACAAAT 2100  
QY 699 AlaGluLeuHisMetAlaThrLysSerCysTrrPileSerGluSerIleGlyValLysValPro 718  
DB 2101 GCTGAATTCACATGGCCACCAAAAGTTGTGTCTCTGAATCATACAGTGTGAAGGTACCC 2160  
QY 719 LysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThr 738  
DB 2161 AAAAGTATAGCAAGTTGGGAGAAATTTACAGATCTAGAGCATGTGGATATCAGGAGACT 2220  
QY 739 SerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThr 758  
DB 2221 AGTACTAGTCATCCAAAGATTTGGCGCAACTTAAGCAAGCTGACTAAATTAAGTGTGACA 2280  
QY 759 ThrAsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaGlyIleSerAspGlyGlyThrLeuGluCys 778  
DB 2281 ACAAAAGGATCCACAGAGGAAAATTTGAAGATCTCTATAGAGCCATCCAAAGGCTCTGT 2340  
QY 779 SerLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCys 798  
DB 2341 TCCCTGCATCTCTCCGTGGATGTGAGGGTCTCTCAGGAATGGAACACTTAATGT 2400  
QY 799 LeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeu 818  
DB 2401 CTAGATCTCTATTCCTATCT 2460  
QY 819 GluGluMetProAsnTrrPileGluGlnLeuThrHisLeuLysLysIleTrrLeuLeuArg 838  
DB 2461 GAGAGATGCCCACTGGATTTGAGCAGCTCTGCCACCTCATGAGTCTTACTTATTAGGG 2520  
QY 839 SerLysLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetVal 858  
DB 2521 AGTAAACTAAAGGAGGAAAAAACCATGCTGATCTTGGGGCATTTGCCAACCTCATGCTGT 2580  
QY 859 LeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPhe 878  
DB 2581 CTTTGTCTTCACTTGTATGCTTACCTCGGAGAAATCTAGTATTTCAGACAGAGCATTC 2640  
QY 879 ProAsnLeuArgThrLeuTrrPileTyrGluLeuAspGlnLeuArgGluIleArgPheGlu 898  
DB 2641 CAAAAGCTCAGACACACTTTGTTTGAACAGCTGGATCGATTAAGAGAGATTAGTTAGG 2700  
QY 899 AspGlySerSerProLeuLeuGluLysIleGluIleGlyCysArgLeuGluSerGly 918  
DB 2701 AACGACAGCTCGCCCTTATTGGAAAAGATAGGAATCCGATCTGCGAGTTGGAAATAGGG 2760  
QY 919 IleThrGlyIleIleHisLeuProLysLeuLysGluIleProIleArgTrrGlySerLys 938  
DB 2761 ATTATTGTATCTCTCACTTATGAGGCTAAAGGAAATTTACACTTGGATACAGATTAA 2820  
QY 939 ValAlaGlyLeuGlyGlnLeuGluGlyValValAsnAlaHisProAsnArgProValLeu 958  
DB 2821 GTTGTGTATCTTGTGTAGTTGGAAAGAGAGATTGGCACACACCAATTCGCCCGTGTCTA 2880  
QY 959 LeuMetTyrSerAspArgTyrHisAspLeuGlyValAlaGluAlaGluGlySerIle 978

Db 2881 CGTATGAGGAGGAGCAGGAGCTGTCTCAGACCTGAGAGGAGGATGCCAAGGATCAGCTGTA 2940

Qy 979 GluValGlnThrAlaAspProValProAspAlaGlu 990

Db 2941 GAAATGGAAGCAAGGAGCCCTCCCTGAGCCGAG 2976

## RESULT 11

US-10-352-179-90

; Sequence 90, Application US/10352179

; Publication No. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

; FILE REFERENCE: 22727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 90

; LENGTH: 3220

; TYPE: DNA

; ORGANISM: Oryza minuta

US-10-352-179-90

## Alignment Scores:

Pred. No.: 2,96e-292 Length: 3220

Score: 3205.50 Matches: 667

Percent Similarity: 74.4% Conservative: 133

Best Local Similarity: 62.0% Mismatches: 202

Query Match: 60.8% Indels: 76

DB: 6 Gaps: 11

US-10-656-394A-8 (1-1032) x US-10-352-179-90 (1-3220)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIleVala 20

Db 1 ATGCGCGATACAGTACTCAGCAATTCGAAGTCCCTGCTGGGAAAGTCTGTGAGCAAGTT 60

Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluIleAspIleTyr 40

Db 61 GCTTCGTTGCCGAGACCAAGATGATCATGCTGCTGGAGTGCAGAGGAGATATGTTTC 120

Qy 41 IleIleAspGluLeuIleThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIleIys 60

Db 121 ATCAAGATGAGCTACAAACGATACAGCATTTTGTGTTGATGCTGCCGAA---GCATCAAG 177

Qy 61 LysAspGluLeuIleValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80

Db 178 AAAAGCATACTATTGAAGTTTGGGTGCAGCAAGTAAGGATCTTTCCTATGACATTGAA 237

Qy 81 AspSerLeuAspGluPheIleValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100

Db 238 GATTGCTTGTGAATTTACAGTTTCATGTCGGCAGCCAAACTGTGCGAGCGAGTTGATG 297

Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuIleSerArgValGlu 120

Db 298 AAGCTAAAGAGTCGCATCGGATTCGCATCCAGATCCGCAATCTCAGGCAAGAAATTGAA 357

Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValIys---ProIleSerSerGlyThr 139

Db 358 GAAGTAAGCACTAGGAACATACGCTACAACTTAATAGAAATGAAATGACCTACCTGCCACCT 417

Qy 140 GluIleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159

Db 418 ACTGATGAGAGGAATTTATTATGGAAGACATTCGCAACCAATAAGCTAACCAACTGNG 477

Qy 160 GluAlaGluLeuValGlyPheSerAspSerIleIysArgLeuLeuGluMetIleAspThr 179

Db 478 GAAGCTGATCTTGTGGGTTTTCTGGACCCCAAAAGAGAGTTGCTTATCTTATAGATGTC 537

Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyIys 199

Db 538 CATGCCAATGACGCGACCTACAAAAGTTGTATGTGTGTCGTATGGGTGGGTAAG 597

Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219

Db 598 ACTACTATTGCAAGGAAATTTATGAAGCAAGAGGACATTCGAAAGATTTTCTTGC 657

Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIle 239

Db 658 TGTGCTTGCAATTACTGTTTTCACAGTCTCTTTGTAGGTTGGAATCTACTCAAGGATTTGATG 717

Qy 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyIysVal 259

Db 718 GTGAACATTTTGGAGAGGAGTACTGAAGAGCGGCTGAGAGAACTCGAAGGGAAG--- 774

Qy 260 ValValGlnValHisLeuSerGluTyrLeuIleGluLeuLeuLysArgTyr 279

Db 775 GTTCCACAAGTAGACGACCTCGCCAGCTACTCAGGACAGAGTAAATGAAAGAGGTAC 834

Qy 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299

Db 835 TTTGTTGCTTGATTAAGTGTGGAGTACAGATTCTGGAATGGATTATAGTAGTTGCC 894

Qy 300 PheProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeu 319

Db 895 TTCCCTAGAAATAACAATAAAGGAGCGCGGTGATAGTAACAACAAGAGATGTTGCTTA 954

Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAsp 339

Db 955 ACTAAGGAGTGTACTTCTGAATTCTTACTACAGTCTTAACCCCTAGAAATAAAGTAT 1014

Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359

Db 1015 GCAAAAGAGTTGCTTCTACGAAAGCAATAAAGCAATAGGAGATATGGAAGTGTATAA 1074

Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379

Db 1075 AGATGAGTGACATTATACTAAATAATTAAGAAGTGTGGCTATTATTACCGTGGCTATA 1134

Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpIleLysPheTyrGlu 399

Db 1135 CTCACAAATAGGAGCGTCTTCCACCAAGAGATAAGAGAGTGGGAAACTTTTATAGT 1194

Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThr 419

Db 1195 CAGATACCTTCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAGGATAGTGACC 1254

Qy 420 LeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhe 439

Db 1255 CTAAGTTACAATCTACTTACCGTCTCATCTTAAAGCAATGCTTTTGTATCTAAGCATATT 1314

Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGlyPhe 459

Db 1315 CCTGAGGATTTTGAATTAATAGAACCGTCTCGTAAATAGATGATGTCAGAGGGGTTT 1374

Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyLysSerTyrPheAsnGluLeu 479

Db 1375 ATTAAGCTAGGACATAATATGACTATTTGAAGATGTTGGGAAAGTTACTTTAAGAACTT 1434

Qy 480 IleAsnArgSerMetIleGlnArgSerArgValIleAlaGlyLysIleIysThrCys 499

Db 1435 ATCAACCGTAGCATGATTTCCAGCCATCAAGAGCGGGTATACGAGGAGATTTTAAAGAGTGT 1494

Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519

Db 1495 CGAGTCCACGACATCATCGTGTATTTACAAATTCGATTTCTAGAGAGAAATTTTACA 1554

Qy 520 LeuLeuProMetGlyAspGlySerAsnLeuValGlnGluAsnThrArgHisIleAlaPhe 539

Db 1555 CTCATTACCCGATGTCAGTCTACTATGATGTAGTACATGGGAACACCTCGGCACATAGAATTT 1614

Qy 540 HisGlySerMetSerCys---LysThrGlyLeuAspTrpSerIleIleArgSerLeuAla 558

Db 1615 CACGGAGTAAAGTATCTCTGAAACAAAGCTTGAGCTGAGCAATATATACGGTCAATTAAC 1674  
Qy 559 ILePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMet 578  
Db 1675 ATGTTTGGTGGAGAGTCCGTAGAACTAGAGCAATTCAGTTTGTTCATCTCAGTTCAGGATG 1734  
Qy 579 LeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArg 598  
Db 1735 TTACGGGTCTTGGATCTTAACAGATGCAATTTCTTATCACAAATATGATGTGCAAC 1794  
Qy 599 ILeAlaLeuLeuCysHisLeuLysTyrLeu-SerIleGlyTyr-----SerSerSe 615  
Db 1795 ATAGTGCTCTGTGCCACTTGAATACCTATGCAATTAAGATACAGATACCTGTTCAACATA 1854  
Qy 615 rIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetPr 635  
Db 1855 TATTTATTCATCTCCAAATCCATAGCTAGCTGCACTGCTGCGAGACATTTGGACTTGGG 1914  
Qy 635 oSerThrTyrIleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLe 655  
Db 1915 TCAGAGTACATTTCAACATGCGCACTGCACTAGATTACTAA-CTTCGGAGTCTCCGAGCCT 1973  
Qy 655 uArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysII 675  
Db 1974 TCGATGATGAAGATATATTTCTTCTTCTTAAACA-----ACATATTT 2018  
Qy 675 eThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspAspArgAl 695  
Db 2019 AACTTAACACATATGCTGCGCATGATATTCACACCTTTCGTTAGTACTCGGATCGTTC 2078  
Qy 695 alyeGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyVa 715  
Db 2079 TGAACCAATTTGCTAAATGACATGCGCCAAAGGCTTCCGTTCAAAATCAAAATGGTGT 2138  
Qy 715 llyValProLysGlyIle---GlyLysLeuArg-AspLeuGlnValLeuGluTyrVala 734  
Db 2139 CAAGTACCAAGGATATGTAATTAATAAATACTGCACTTACAAATATGAGGATGTTGG 2198  
Qy 734 spIleArgArgThrSerSerArgAlaIleLysLeuGluGlyGlnLeuSerLysLeuArgL 754  
Db 2199 ATATTAGAGGACTAGCAGTAGAGCAATCAAGAGTTGGGGCAGTTAAGCAAGCTGAGGA 2258  
Qy 754 yLeuGlyValThrThrAsnGlySerThrLysGlyLysCysLysIleLeuTyrAlaAlaI 774  
Db 2259 AATTATGTGTGTAACAAAGGATCCAAAGGAAATGAGAGATCTTATACAGCTA 2318  
Qy 774 leGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyLysSerAspGlyG 794  
Db 2319 TCCAGAGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2378  
Qy 794 lyThrLeuGluCysLeuAspSerLysSerProProLeuLeuArgThrLeuValL 814  
Db 2379 GAACATTCAGTGTATGATATCTTATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438  
Qy 814 euAspGlyIleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysI 834  
Db 2439 TGAATGGAAGCTTTGAGGAGATGCTTAACCTGATGCTGAGGATTTTCAGGTATTG 2498  
Qy 834 leTyrLeuLeuArgSerLysLeuLysGlyLysThrMetLeuIleLeuGlyAlaLeuP 854  
Db 2499 TCAACTTATGAGAGGAGCAATTAAGAGGTAATTAACCAATGTTGATCTTCGGCGGTGC 2558  
Qy 854 roAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheL 874  
Db 2559 CCAACCTCATGCTCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2618  
Qy 874 yThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGlnLeuAspGlnLeuArgG 894  
Db 2619 AAATGGGAGCAATCCCAAAATCTTAGAACATTTTCGATTTTACAAATTTGAGCAGCTAAG 2678  
Qy 894 luIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIleGlyLysCysA 914

Db 2679 AGATTAGATTGAGGACGCGAGCTCAATCTTCTTGGAAAGATAGAAATATT-CAG---G 2734  
Qy 914 rgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGluIleProIleA 934  
Db 2735 GGTGGAAATCAGGAGATTGTTGGTATCATTTACCTTTCAAGGCTCAAGGAGATTTCACCT 2794  
Qy 934 rgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyValAsnAlaHisProA 954  
Db 2795 GATACGGAAGTAAGTGGCTAGGCTTGGTACGCTGGAGGAGAGTGGCGACACACCCAA 2854  
Qy 954 snArgProValLeuLeuMetTyrSerAspArgTyrHisAspLeuGlyAlaGluAlaG 974  
Db 2855 ATACCCCGGTGCTGCAATGAGGAGGACGGAAGTATCAGACCTTCTTGTGACGCG 2914  
Qy 974 luGlySerSerIleGluValGlnThrAlaAspProValProAspAlaGluGlySerValT 994  
Db 2915 AAGATCCCTGTTGAA----- 2931  
Qy 994 hrValAlaValGluAlaThrAspProLeuProGluGlnGluGlyGluSerSerGlnSerG 1014  
Db 2932 -----GTGGAAGCAACAGATCCTGT-----GAGAGCTCACAGTTGC 2967  
Qy 1014 lnValIleThrLeuThrThrAsnAsp----- 1022  
Db 2968 AGGTGATCATCGTTGCAACGAACGACAGGTCACTCCTTACACGCGCATCTTAATGAA 3027  
Qy 1022 ----- 1022  
Db 3028 CTGTTTATCTCTTGTGAGATCGATGATTTTAACCTACCTTTCATCTCTCTGTTT 3087  
Qy 1023 -----SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3088 CTTAACCTAACACGGAAGAGATAAGCACTTAAGCTGTGT 3128

## RESULT 12

US-10-656-394A-5  
; Sequence 5, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; TITLE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4147  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1983)  
US-10-656-394A-5

## Alignment Scores:

Pred. No.: 1,68e-285 Length: 4147  
Score: 3136.00 Matches: 676  
Percent Similarity: 63.0% Conservatives: 126  
Best Local Similarity: 53.1% Mismatches: 200  
Query Match: 59.5% Indels: 274  
DB: 8 Gaps: 11

US-10-656-394A-8 (1-1032) x US-10-656-394A-5 (1-4147)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 1 ATGCGGATACACTACTCAGCAATTCGAAAGTCCCTCGTGGAGAGTCTGTAGCAAGTT 60  
Qy 21 AlaserAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTyr 40  
Db 61 GCTTCGGTCCCGCAGACAAGATGATGCTGCTGGGAGTGCAGAGGATATGTTTC 120



Db 2259 GGATGGGTAGGATCGGAGAGAAAGATGAGCAAGGGTGGATGATGAGGAGTACCTGTTTCG 2318  
QY 725 ----- 725  
Db 2319 AGTCGTCTTCCCGCGCGCGCGCGGTGGAGTACCTGTTTCGAGTCGTCTGTTCCCGG 2378  
QY 725 ----- 725  
Db 2379 TGGCGGCGAGAGCAACAAGGAGCGCGCGCGCGCGGAGAGGATAAAGTCCGGCGGAG 2438  
QY 725 ----- 725  
Db 2439 CCGAG 2498  
QY 725 ----- 725  
Db 2499 CGGCGAAG 2558  
QY 725 ----- 725  
Db 2559 CCAGCGTAGTGGGTTGAGCGCGCGCGCGAGTCCAAACCCATCTATTGACGCGAGTTACT 2618  
QY 725 ----- 725  
Db 2619 CTTTACCCTTCCAACTCTCTTCTCATGCGGTATCACCTAAGGAGACATTTTGTGTACCG 2678  
QY 725 ----- 725  
Db 2679 TCGGTACACGCAACATCAGCGCTTGGATCAGCGCGAGATCCACGCGCAGCATTTGGTA 2738  
QY 726 ----- 726  
Db 2739 CGGCTCGGTACGTTGGACAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2798  
QY 735 eArgArgThrSerArgAlaIleLysGluLeuGlnLeuSerLysLeuArgLysLe 755  
Db 2799 TAGAAGGACTAGCAGTAGAGCAATCAAGAGATGGGGCAGTTAAGCAGCTGAGGAAT 2858  
QY 755 uGlyValThrAenGlySerThrLysGluLysCysLysIleLeuTyAlaAlaIleG 775  
Db 2859 ATGTGTGTAAACAAAGGAGATCCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2918  
QY 775 uLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyL 795  
Db 2919 GAAGCTCTGTTCCTACAACTCTCCATGTGAATGCTGTGGAGTTTCAGGTATGGAAC 2978  
QY 795 rLeuGluCysLeuAspSerLysSerSerProProLeuLeuArgThrLeuValLeuAs 815  
Db 2979 ACTTCAGTGATAGATCTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3038  
QY 815 pGlyLeuLeuGluMetProAenThrLleGluGlnLeuThrHisLeuLysLysIleTy 835  
Db 3039 TGGAAAGTCTTGAGGAGATGCTTAACCTGATGAGCAGCTACGACCTGATGAAGTTCAA 3098  
QY 835 rLeuLeuArgSerLysLeuLysGluLysThrMetLeuLeuLeuGlyValaLeuProAs 855  
Db 3099 CTTATGGAGGAGCAACATAAGAGAGTAAACCAATGTTGGTACTTGGCGGTGCCCAA 3158  
QY 855 nLeuMetValLeuHisLeuTyArgAenAlaTyLeuGluLysLeuValPheLysTh 875  
Db 3159 CCTCATGTGCTCTTATCT 3218  
QY 875 rGlyAlaPheProAenLeuArgThrLeuThrLleTyGluLeuAspGlnLeuArgGlu 895  
Db 3219 GGGAGCATCTCCCAATCTTAGACATTTTCGATTTTACAAATTTGGACAGCTAAGAGAT 3278  
QY 895 eArgPheGluAspGlySerSerProLeuLeuGluLysLysIleGluLysGluCysArgLe 915  
Db 3279 TAGATTGAGGACGCGCAGCTCAATCTTGTGGAAAGATAGAAATATT-CAG---GGGT 3334  
QY 915 uGluSerGlyIleThrGlyLleIleHisLeuProLysLeuLysGluIleProIleArgTy 935

Db 3335 GGAATCAGGAGTGTGTTGGTATCATTCACCTTCAAGGCTCAAGGAGATTTCATTGGATA 3394  
QY 935 rGlySerLysValaIleLysLeuGlnLeuGluGlyGluValAsnAlaHisProAsnAr 955  
Db 3395 CGGAAGTAAAGTGGCTAGGCTTGGTCACTGGAGGAGAGAGTGGCGCAACATCA 3454  
QY 955 gProValLeuLeuMetTyrSerAspArgArgTyrHisAspLeuGlyAlaGluAlaGlu 975  
Db 3455 CCCGCTGATCGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3514  
QY 975 ySerSerIleGluValGlnThrAlaAspProValProAspAlaGluGlySerValThrVa 995  
Db 3515 ATCCCTCTGTGAA----- 3527  
QY 995 lAlaValAlaAlaThrAspProLeuProGluGlnGluGlyGluSerSerGlnVa 1015  
Db 3528 ---GTGGAAGCAACAGATCTCTG-----GAGAGCTCGAGTTCCAGGT 3567  
QY 1015 lIleThrLeuThrThrAsnAsp----- 1022  
Db 3568 GATCACGTTGACAAACGAGACGAGGTCACTCCCTACACGGCATCTTAATGAACTTG 3627  
QY 1022 ----- 1022  
Db 3628 TTTTATCCTTGTGAGATCGATGATTTTAATCACCCTTTCATCTCTCTGTTTCTTA 3687  
QY 1023 -----SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3688 ACCTAACAGCGAGAGATAGACACAACTTAAGCTGTGT 3724

RESULT 13  
US-10-656-394A-1  
; Sequence 1, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; TITLE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2982)  
US-10-656-394A-1

Alignment Scores:  
Pred. No.: 1,15e-279 Length: 2982  
Score: 3072.00 Matches: 614  
Percent Similarity: 76.5% Conservative: 144  
Best Local Similarity: 62.0% Mismatches: 223  
Query Match: 58.3% Indels: 10  
DB: Gaps: 4

US-10-656-394A-8 (1-1032) x US-10-656-394A-1 (1-2982)

QY 2 AlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAlaAla 21  
Db 7 GCGGAGACGGTGGTGGATGCGGATGCGGTCTCGGCGAGCGCGCTCGGGAAGCGCC 66  
QY 22 SerAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTyIle 41  
Db 67 TCGCGCGCGCGGAGAGGAGCGCCCTCTCTGCTCGGATCCAGAGAGAGATCTGGTACATC 126  
QY 42 LysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 61  
Db 127 AAGGACGAGCTGAAACATTAATTCAGGATCTTAAGAGCTGCTGAAGTAAACAAGAAGAA 186

Qy 62 AspGluLeuLeuValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluLeu 81  
Db 187 GATGACCTGCTAAAGGTATGGCGACAGAGTACGAGATCTGTATATACATTAAGAT 246  
Qy 82 SerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLys 101  
Db 247 TGCCTAGACGAATTCAGGTTCACTGTTGAGAGCCAAAGCTTGGCAAGCACTATGAG 306  
Qy 102 LeuArgGluArgHisArgIleAlaIleArgIleHisIleLeuValLysValGluGlu 121  
Db 307 CTTGGTGAACGCCATCGAATGCTGTACAGATTCGCAACTTAAATCAAGAAATGAGAA 366  
Qy 122 ValSerArgAsnThrArgTyrSerLeuValLysProIleSerSer--GlyThrGlu 140  
Db 367 GTGAGCAACAGGAAATACAGCTACAGCTTAATCAAGCCATTTCTCTATACCAAGAG 426  
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgHisGlnSerAlaArgHisValAspGlu 160  
Db 427 GATGAGAGGATTCCTACTAGAGATGCTCGCAATCGATCAGTACCAACTGACGAG 486  
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 487 TCGAACTTGTGGGCTTTCGCAAGCTAAAGATGAGTGTCTTAACCTGATGATGCAAT 546  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 547 ACTAATGACGGTCCAGCTAAAGTGTATGTGTGGTGTGATGCGGTGATGAGCAAGACT 606  
Qy 201 AlaLeuSerArgLysPheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 607 ACCCTTGCAGGAGGAGGATATGAACACAGGACACATG--AAGAACTTCTCGTGTGT 663  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 664 GCTTGGATCACTGTGTCTCAGTCACTTTGACAGGAAGAAATCTGAAACAAATGATCAGG 723  
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnLeuGlnGlyLysValVal 260  
Db 724 CAACCTCTGGGTGCTGATTCATTAGACAACTCTTGAAAGAAATTTAGTGAAGATGTCTC 783  
Qy 261 ValGlnValHisLeuSerGluTyrIleGluLeuLeuLysGluLysArgTyrPhe 280  
Db 784 GTGCAAGTCCAGCATCTCGTGTACCTGTGTGTTGAGGGCTAAAGGAGAAAGTACTTT 843  
Qy 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 844 GTTGTCTTGTGACCTATGACCATAGATGATGCAATGGAATTTGGAATTCATGATATGCTTT 903  
Qy 301 ProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
Db 904 CCGAAGATTAAACACAGAGGTAGTCGCATAATAACACGCGAGATGCTGGCTTAGCT 963  
Qy 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 964 GGAAGGTGTACCTCGAATCACTATTATACCCCTGGAACCGTTACATATGATGATGCT 1023  
Qy 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1024 ATACACTTGCTACTAGCAACAGACAAACATAAGACTTGAAGACATGGAATGATGAGGAC 1083  
Qy 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1084 TTGGGCAGCATAGTTACAAATTTGGTGAAGGTGTGGTATTATACCGTGTGCTATCTC 1143  
Qy 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGlnLysPheTyrGluHis 400  
Db 1144 ACAATAGGAGGCACTTCTTGTCTACTAAGAGATATGAGTGGGGGAAATTTTACAGAA 1203  
Qy 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeu 420  
Db 1204 CTTCTCTCAGAGCTTTGAGAGCAATCCCAAGCTTAGAGCCATGAGGAGGATGTTGACCTTA 1263

Qy 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
Db 1264 AGCTCAATCACTTACCATCTCATCTTAAACCACTGCTTTCTTACCCTAAGTATTTTCCCT 1323  
Qy 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1324 GAAGATTTGAATTTCAAGAGGGCGCTGCTAGATAGATAGATAGATAGATAGATAGAT 1383  
Qy 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeu 480  
Db 1384 AGAGCCACAGATGGGGTGAACATTTGAGGATGTTGGAATAGTACCTTTTATGAGCTTATC 1443  
Qy 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1444 AACAGATCTGATTCAGCCCTCAAAAGTTAGTACAGATGGATGCTTAAAGAGATGCTGA 1503  
Qy 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeu 520  
Db 1504 ATCCATGATATCATGCGTGTATCATATGTTTCAATTTCTAGAGAGGAAATTTTGTGCTG 1563  
Qy 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
Db 1564 TTGACTAGGAGAGATCCTGTTGTAGCGAGAGAGATCCGCCATCTAGCATTTCTAT 1623  
Qy 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleArgSerLeuAlaIlePhe 560  
Db 1624 GGGAGCAAAATGCTCAAAAGATATGCTTGGAGTGAACCATCTGCGCTCAGTAATTTGTTT 1683  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1684 GCGACACACCTGTGGGCGACACCTGCGCTTTGTTCCACCATTTAGGATGCTGAGA 1743  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1744 GTGTTGGATCTGGAAGATGCAAAATTTCAAAATTCACACAAATGATATCAGAAATATAGG 1803  
Qy 601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1804 TTGTTGCCACATCAAAATTTGAAATTTGAAATTTGCAAGAGCTTCAACTATTATTACATTC 1863  
Qy 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1864 AGGTCCATAGGAAATTTGCAGTGTCTGCAAAATTTTGAACATGAGGAGGCAAAATCTCA 1923  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1924 GCACCTAACACTGAGGTGACTTAACTCCAGATCTCCGATGCTCCGATGCGAGGAGG 1983  
Qy 661 PheHisTyrAspAsnPheSer--LeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 1984 TCTGTTCTGTTACTTTAGCATATAGATATATCCCAAGGAATGCTTGATGATCACCATG 2043  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAla 699  
Db 2044 TGTCTTACGATGGTTTCTTAACTTCAATAAATTTTCAAGTGTGAGTGAATTAATCTCT 2103  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 2104 GAGATATGATGTCATGCTCTCTCCCTGCTCTGATACAAAGGGTGTGAGGGTGTGCAAGA 2163  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSer 739  
Db 2164 GGAATTTGACACCTTAAAGAGTTACAGATCTTAGAAGTCTGATGATCAACAGAACTAGT 2223  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThr 759  
Db 2224 AGGAAGCGCATTTGAAGAGCTGGGGAGCTAAATTCAGTTAAGAAATTTAAGCGTGAACA 2283  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSer 779  
Db 2284 AAAGCGCCCAAAATAGAAAGTATCAGATATTTTGTGACGAGGATTTGAGAGCTCTCTCT 2343  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799









LENGTH: 2940  
 TYPE: DNA  
 ORGANISM: Oryza minuta  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(2940)  
 OTHER INFORMATION:  
 US-10-352-179-84

Alignment Scores:

Pred. No.: 7,19e-279 Length: 2940  
 Score: 3063.50 Matches: 611  
 Percent Similarity: 77.4% Conservative: 141  
 Best Local Similarity: 62.9% Mismatches: 217  
 Query Match: 58.2% Indels: 3  
 DB: 6 Gaps: 3

US-10-656-394A-8 (1-1032) x US-10-352-179-84 (1-2940)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
 Db 1 ATGGCGGAGACGGTGGTGGATGCGGATGCGGTCGGGAGCGCGCGTGGGAGGCC 60  
 Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluLeuAspIleThr 40  
 Db 61 GCCTCCGCGCGCGGAGGAGGCGCCCTCTGCTGGGCTCCAGAGGAGATCTGGTAC 120  
 Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLys 60  
 Db 121 ATCAAGGACGAGCTGAAACTATTTCAGGCATCTTAAAGCTGCTGAAGTAAACAAGAG 180  
 Qy 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyAspIleGlu 80  
 Db 181 AAAGATGACTTGTAAAGGTATGGGAGGAGCAAGTACGAGATCTGTCTATAAATGAA 240  
 Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
 Db 241 GATTGCTTAGAGCAATTCAGGTTCAAGTTGAGGCAAGCTTGGCAACCAACTAATG 300  
 Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
 Db 301 AAGCTTGTGTGAACGCCATCAATTCGTGTACAGATCTCAACTTAAATCAAGAATGAA 360  
 Qy 121 GluValSerSerArgAnthrArgTySerLeuValLysProIleSerSer---GlyThr 139  
 Db 361 GAAGTGAACAACAGGATACACGCTACAGCTTAATCAGCTCATTTCTCTATACACCA 420  
 Qy 140 GluIleAspMetAspSerTyAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159  
 Db 421 GAGGATGAGAGGGATTCCTACCTAGAGATGCTCGCAATCGATCAGGTAGCAACACTGAC 480  
 Qy 160 GluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThr 179  
 Db 481 GAGTCAGAACTTGTGGGCTTTGGCCAGACTAAAGATGAGTGTCTTAAACTGATAGATGC 540  
 Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLys 199  
 Db 541 AATACTAATGACGCTCCAGCTAAGTGATATGTTGTTGGAATGGGTGGATTAGGCAAG 600  
 Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219  
 Db 601 ACTACCTTGCAGGAAGGATATGAAGAAACAGGAAACACATG---AAGAACTTCTCGTGT 657  
 Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239  
 Db 658 TGTGCTTGATCACTGTGTCTCAGTCACTTTGACAGGAAGAATACTTGAACAATGATC 717  
 Qy 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluGlnGlyVal 259  
 Db 718 AGGCAACTTCTGGGTGCTGATTCATTAGACAAACTCTTGAAGAATTTAGTGAGAAGTTG 777  
 Qy 260 ValValGlnValHisLeuSerGluThrLeuIleGluLeuLysGluLysArgTy 279

Db 778 CTGTCGCAAGTCCAGCATCTCGCTGATCCTCTGGTTGAAGCGCTAAAGAGAAAAGGTAC 837  
 Qy 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299  
 Db 838 TTTGTTGTCCTTCGATGACCTTATGGACCATAGATGATGGAATTTGATTCATGACTGCT 897  
 Qy 300 PheProLysAsnAsnLysLysGlySerArgIleValIleThrArgAsnValAspLeu 319  
 Db 998 TTTCCGAGATTAAACAACAGAGGTAGTCATATTAATTAACAACGCGAGATGCTGGCTTA 957  
 Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyHisLeuAspPheLeuGluMetAsnAsp 339  
 Db 958 GCTGGAAGGTGATCTCTGAATCACTATTATACCACCTTGAACCGTTCATATATAGATGAT 1017  
 Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
 Db 1018 GCTATACACTTGTCTACTGCAAGACAAACATACACTTGAAGACATGGAANAATGATGAG 1077  
 Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
 Db 1078 GACTTGGGAGCAGTAGTACAAAATTTGGTAAAGAGGTGGTATTATTTACCCTGGCTATA 1137  
 Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyGlu 399  
 Db 1138 CTCACAATAGAGGCAATCTTCTACTAAGAAATTAATGGAATGGGNAATTTTACAGA 1197  
 Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThr 419  
 Db 1198 GAACCTCTTCAGAGCTTCAGAGCAATCCAGCCCTAGAAGCCATGAGGAGGATGGTGACC 1257  
 Qy 420 LeuGlyTyAsnHisLeuProSerHisLeuLysProCysPheLeuTyLeuSerIlePhe 439  
 Db 1258 CTAAGCTACAACTACCTTACCTCATCTTAAACCATGCTTCTTTTACCTAAGTATTTC 1317  
 Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
 Db 1318 CCTGAAGATTTTCAAAATTCAAAGAGGCGCTCTGGTGTAGATAGATGATGATGAGGGTTT 1377  
 Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyPheAsnGluLeu 479  
 Db 1378 GTCAAGGCCACAGATCGGTGAACTTGAAGATGTTGGAATAGTCTCTTAAATGAGCTT 1437  
 Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
 Db 1438 ATCAACAGAGATCTGATTCAGCCCTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGT 1497  
 Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
 Db 1498 CGAATCCATGATATCATGCTGATATCATAGTTTCAATTTCTAGAGAGGAAAAATTTGTG 1557  
 Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
 Db 1558 CTGTTGCTAGGAGAGATCACTGTTGTAGCGGAGGAGAGATCCGCCATCTAGCATTT 1617  
 Qy 540 HisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
 Db 1618 CATGGAGCAAAATGCTCAAAAGATAGTCTGGAGTGGAAACCATCTCGCTCAGTAACCTTG 1677  
 Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
 Db 1678 TTTGGTACAGACCTCGCGGGGGAACCTGCACTTTGTTCCACCACAATTTAGGATGCTG 1737  
 Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
 Db 1738 AGAGTGTGATCTGGAAGATGCAAAATTCAAAATTCACACAAAATGATATCAGGAATATA 1797  
 Qy 600 AlaLeuLeuCysHisLeuLysTyLeuSerIleGlyTySerSerSerIleTySerLeu 619  
 Db 1798 GGGTGTGTGCGCACATGAATATTGAAATTTTGCACAGAGCTCACTATTATTACACTT 1857  
 Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIle 639  
 Db 1858 CCAAGGTCCATAGAAAAATTCAGTGTGCTTGCATAATTTTGAACATGAGGAGGCAATATC 1917

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Oy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659
Db 1918 TCAGCACTAACAACTGAGGTGACTTAACTCCAGAACTCTCGTAGCTCCGATGCAGCAGG 1977
Oy 660 GlnPheHisTyrAspAsnPheSer--LeuAsnHisProMetLysCysIleThrAsnThr 678
Db 1978 AGGTCAAGTTCCTGGTTACTTTAGCATATATAGATAATCCCAAGAAATGCTTGATATCACC 2037
Oy 679 IleCysLeuProLysValPheThrProLeuValSerArgAspArgAlaLysIle 698
Db 2038 ATGTGCTTACCGATGGTTTCTCAACTTCAATAAATTCAGTGCACCGTGTGAAGTTAAT 2097
Oy 699 AlaGluLeuHisMetAlaThrLysSerCysTyrSerGluSerIleGlyValLysValPro 718
Db 2098 CCTGAGATATCATGTATGTTCTACCCGTGGTCTGTATACAAAGGGTGTGAGGTGCCA 2157
Oy 719 LysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThr 738
Db 2158 AGAGGAATTTGACAACTTAAAGAGATTACAGATTCTAGAAGTCTGTGCATCAACAGAACT 2217
Oy 739 SerSerArgAlaIleLysLeuGlnLysLeuSerLysLeuArgLysLeuGlyValThr 758
Db 2218 AGTAGAAGGCGCATTTGAAGAGCTGGGGAGCTTAATTCAGTTAAGAAATTAAGCGTGACA 2277
Oy 759 ThrAsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSer 778
Db 2278 ACMAAGGCGCCACAAATAAGAGTATCAGATATTTTGTGCAGCGATTGAGAGCTCTCT 2337
Oy 779 SerLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCys 798
Db 2338 TCTCTGCAATCTCTCCGTGGAGTGTGAGGGATTCTCAGATACCTGGAACACTTTGAGTGG 2397
Oy 799 LeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeu 818
Db 2398 CTCATTCGATTGTCATGCTCTCTCCATTCTTGAAGACACTCAAGTTCAGTGAATGATCTCT 2457
Oy 819 GluGluMetProAsnThrIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArg 838
Db 2458 GCAGATACACCAAACTGGTTGGGAACCTTTAAGCAGCTGTGTGAAGATGTGCTTATCCAGA 2517
Oy 839 SerLysLeuLysGluLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetVal 858
Db 2518 TGTGTGCTTACAAGATGTATAAACTATGGAGATACTTTGGGGCACTGCCCACTTATGTT 2577
Oy 859 LeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPhe 878
Db 2578 CTTCGTCTTTATCGCAACGCATATGCTGCAGAGAAATGGCAATTCAGAGGGGGAACATC 2637
Oy 879 ProAsnLeuArgThrLeuThrIleTyrGluLeuAspGlnLeuArgGluIleArgPheGlu 898
Db 2638 CCAAACTCTCAGGTCTCTTGATATTTACTTGTGTAAGCAACTTAGAGAGATAAGATTGAG 2697
Oy 899 AspGlySerSerProLeuGluLysIleGluIleGlyGluCysArgLysLeuGluSerGly 918
Db 2698 GAGGCACTCTGCCCAACAACTGTAAGATATAGAAATTTATGTTGAGGTTGGAATCAGGG 2757
Oy 919 IleThrGlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyrGlySerLys 938
Db 2758 AFTATTGGTATCAAGCACTTCCAGACTTTAGATTATTTCCGTTGAATATGATGTTAA 2817
Oy 939 ValAlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeu 958
Db 2818 GTCGCAAGCTTGTATGTGTCGAAGAGGAAGTGAATACACACCCCAATCATCTACTGAACTG 2877
Oy 959 LeuMetTyrSerArgArgTyrHisAspLeuGly 970
Db 2878 CAATGGCAGAGGATCGAAGTCATCATGACCTAGGA 2913
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Search completed: March 9, 2006, 23:23:39  
Job time : 1957 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 9, 2006, 22:52:26 ; Search time 2260 Seconds  
(without alignments)  
1053.598 Million cell updates/sec

Title: US-10-656-394A-8  
Perfect score: 5268  
Sequence: 1 MAEVLVSMARSLVGSALSKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 1153648444 residues  
Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-O=/abs/ABSSWEB spool/US10656394/runat\_09032006\_094027\_822/app\_query.fasta 1  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=absos3p  
-USER=US10656394 @CGN 1 1 653 @runat\_09032006\_094027\_822 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US05\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	668.5	12.7	2151	9 US-11-031-206-125	Sequence 125, App
2	541.5	10.3	1861	9 US-11-031-206-115	Sequence 115, App
3	524	9.9	1944	9 US-11-031-206-109	Sequence 109, App
4	474	9.0	1902	9 US-11-031-206-137	Sequence 137, App

5	357.5	6.8	813	9	US-11-031-206-127	Sequence 127, App
6	322.5	6.1	4671	9 <td>US-11-096-568A-30746</td> <td>Sequence 30746, A</td>	US-11-096-568A-30746	Sequence 30746, A
7	309	5.9	2382	9 <td>US-11-031-206-101</td> <td>Sequence 101, App</td>	US-11-031-206-101	Sequence 101, App
8	298	5.7	644	9 <td>US-11-031-206-107</td> <td>Sequence 107, App</td>	US-11-031-206-107	Sequence 107, App
9	250	4.7	4585	9 <td>US-11-096-568A-34295</td> <td>Sequence 34295, A</td>	US-11-096-568A-34295	Sequence 34295, A
10	237.5	4.5	629	9 <td>US-11-031-206-133</td> <td>Sequence 133, App</td>	US-11-031-206-133	Sequence 133, App
11	225	4.3	634	9 <td>US-11-031-206-139</td> <td>Sequence 139, App</td>	US-11-031-206-139	Sequence 139, App
12	206.5	3.9	1892	9 <td>US-11-031-206-105</td> <td>Sequence 105, App</td>	US-11-031-206-105	Sequence 105, App
13	203.5	3.9	785	9 <td>US-11-031-206-121</td> <td>Sequence 121, App</td>	US-11-031-206-121	Sequence 121, App
14	187	3.5	306	9 <td>US-11-031-206-123</td> <td>Sequence 123, App</td>	US-11-031-206-123	Sequence 123, App
15	186.5	3.5	549	9 <td>US-11-031-206-119</td> <td>Sequence 119, App</td>	US-11-031-206-119	Sequence 119, App
16	183	3.5	6773	8 <td>US-10-947-249-105</td> <td>Sequence 105, App</td>	US-10-947-249-105	Sequence 105, App
17	169	3.2	3725	9 <td>US-11-096-568A-32720</td> <td>Sequence 32720, A</td>	US-11-096-568A-32720	Sequence 32720, A
18	168.5	3.2	585	9 <td>US-11-031-206-113</td> <td>Sequence 113, App</td>	US-11-031-206-113	Sequence 113, App
19	167.5	3.2	3647	7 <td>US-11-096-568A-31266</td> <td>Sequence 31266, A</td>	US-11-096-568A-31266	Sequence 31266, A
20	163	3.1	5658	7 <td>US-10-932-182A-6026</td> <td>Sequence 6026, App</td>	US-10-932-182A-6026	Sequence 6026, App
21	163	3.1	5658	7 <td>US-10-932-182A-6026</td> <td>Sequence 6026, App</td>	US-10-932-182A-6026	Sequence 6026, App
22	162	3.1	1257	9 <td>US-11-096-568A-29993</td> <td>Sequence 29993, A</td>	US-11-096-568A-29993	Sequence 29993, A
23	161	3.1	10211	12 <td>US-11-000-688-98</td> <td>Sequence 98, App</td>	US-11-000-688-98	Sequence 98, App
24	160	3.0	2943	12 <td>US-11-010-239-126</td> <td>Sequence 126, App</td>	US-11-010-239-126	Sequence 126, App
25	159.5	3.0	2966	9 <td>US-11-072-512-157</td> <td>Sequence 157, App</td>	US-11-072-512-157	Sequence 157, App
26	156.5	3.0	3117	7 <td>US-10-932-182A-2299</td> <td>Sequence 2299, App</td>	US-10-932-182A-2299	Sequence 2299, App
27	156.5	3.0	3117	7 <td>US-10-932-182A-2299</td> <td>Sequence 2299, App</td>	US-10-932-182A-2299	Sequence 2299, App
28	154.5	2.9	3008	12 <td>US-11-010-239-114</td> <td>Sequence 114, App</td>	US-11-010-239-114	Sequence 114, App
29	154.5	2.9	3309	9 <td>US-11-096-568A-27956</td> <td>Sequence 27956, A</td>	US-11-096-568A-27956	Sequence 27956, A
30	154	2.9	17642	8 <td>US-10-995-561-256</td> <td>Sequence 256, App</td>	US-10-995-561-256	Sequence 256, App
31	153	2.9	16792	8 <td>US-10-995-561-262</td> <td>Sequence 260, App</td>	US-10-995-561-262	Sequence 260, App
32	153	2.9	17292	8 <td>US-10-995-561-260</td> <td>Sequence 257, App</td>	US-10-995-561-260	Sequence 257, App
33	153	2.9	17436	8 <td>US-10-995-561-257</td> <td>Sequence 254, App</td>	US-10-995-561-257	Sequence 254, App
34	153	2.9	17507	8 <td>US-10-995-561-254</td> <td>Sequence 258, App</td>	US-10-995-561-254	Sequence 258, App
35	153	2.9	17610	8 <td>US-10-995-561-258</td> <td>Sequence 259, App</td>	US-10-995-561-258	Sequence 259, App
36	153	2.9	19023	8 <td>US-10-995-561-259</td> <td>Sequence 122, App</td>	US-10-995-561-259	Sequence 122, App
37	151.5	2.9	10300	8 <td>US-10-947-249-122</td> <td>Sequence 34461, A</td>	US-10-947-249-122	Sequence 34461, A
38	150.5	2.9	3251	9 <td>US-11-096-568A-34461</td> <td>Sequence 3255, App</td>	US-11-096-568A-34461	Sequence 3255, App
39	150.5	2.9	5127	12 <td>US-11-136-527-3255</td> <td>Sequence 1, Appli</td>	US-11-136-527-3255	Sequence 1, Appli
40	149.5	2.8	14121	9 <td>US-11-200-710-1</td> <td>Sequence 10, Appli</td>	US-11-200-710-1	Sequence 10, Appli
41	149.5	2.8	14121	12 <td>US-11-124-020A-10</td> <td>Sequence 3, Appli</td>	US-11-124-020A-10	Sequence 3, Appli
42	149.5	2.8	14121	12 <td>US-11-123-656A-3</td> <td>Sequence 135, App</td>	US-11-123-656A-3	Sequence 135, App
43	148.5	2.8	590	9 <td>US-11-031-206-135</td> <td>Sequence 349, App</td>	US-11-031-206-135	Sequence 349, App
44	148.5	2.8	2479	7 <td>US-10-973-115B-349</td> <td>Sequence 349, App</td>	US-10-973-115B-349	Sequence 349, App
45	148.5	2.8	2479	8 <td>US-10-131-826A-349</td> <td>Sequence 349, App</td>	US-10-131-826A-349	Sequence 349, App

#### ALIGNMENTS

#### RESULT 1

US-11-031-206-125  
; Sequence 125, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Fomodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; TITLE OF INVENTION: Stress Response  
; FILE REFERENCE: B1357 US NA  
; CURRENT APPLICATION NUMBER: US/11/031,206  
; PRIOR FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437

QY	1	MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla	20
DB	702	ATGGCGAAATGGCAGTGTCTCTCGCAGCA-----GACAATTGG	740
QY	21	AlaSerAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTyr	40
DB	741	CTTCCACTACTAAGCGACGACGAAAACACTGCTTTGGAACATCCCAAGAATTTGAAGC	800
QY	41	IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaIleGluLeuMetLysLys	60
DB	801	ATACAAAATGAATAGATAATCAATTCAAGGCTCCTCGAAGCGCAGATAGAATGGCTGCA	860
QY	61	LysAsp-----GluLeuLeuLysValTIPAlaGluGlnIleArgAspLeu	75
DB	861	GAAGAAGGAGACACGCAAAACAGGGAATCAAAAAATGGTGAAGGACTTTGAGGGAAGCA	920
QY	76	SerTyrAspIleGluAspSerLeuAspGluPheLysValHisIleGluSerGln-----	93
DB	921	TCATTCCGAATAGAAGTGCATTGATGAACAATTATCTATGTGGAAACACCGCTCAT	980
QY	94	-----ThrLeuPheArgGlnLeuValLys	101
DB	981	GATGCTCTGGTTGTGCAGCTTTACTCTTTGATGTGCAATATCATCTCACTTCATGAATCT	1040
QY	102	LeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGluGlu	121
DB	1041	TTGAGGCGTGCATCAAAATAGCATCAGAGATTACAGCAGATTAAGTCAATTGTTCAAAGG	1100
QY	122	ValSerSerArgAsnThrArgTyrSer---LeuValLysProIleSerSerGlyThrGlu	140
DB	1101	ATCAAGCAAAAGGATTGATTATGACTACTACTAATCAAACCT-----TCTCTTGG	1151
QY	141	IleAspMetAspSerTyr-----AlaGluAspIleArg-----AsnGlnSer	154
DB	1152	CACGGATCAAGCAGCTCAGAGGAGGCCAAAGTGTCCAATGCATGACCTCGATTTGGCT	1211
QY	155	AlaArgAsnValAspGluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeu	174
DB	1212	TCACGTTACCTTTGACGAAAGCCGAGTTGTTGGCCCTTGAAGACCCCTAAAGATGAATTTGATA	1271
QY	175	GluMetIleAspThrAsnAlaAsnAspGlyProAlaLys-----ValIleCysValVal	192
DB	1272	-----ACTTGGTTAGTGGAGGACCGACGAGCCGACCATCATCTTTTGTGGTGA	1319
QY	193	GlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGluGluAsp	212

TITLE OF INVENTION: Stress Response  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/11/031.206  
CURRENT FILING DATE: 2005-01-07  
PRIORITY APPLICATION NUMBER: US/09/566.394  
PRIORITY FILING DATE: 2000-05-05  
PRIORITY APPLICATION NUMBER: 60/133038  
PRIORITY FILING DATE: 1999-05-07  
PRIORITY APPLICATION NUMBER: 60/133042  
PRIORITY FILING DATE: 1999-05-07  
PRIORITY APPLICATION NUMBER: 60/133427  
PRIORITY FILING DATE: 1999-05-11  
PRIORITY APPLICATION NUMBER: 60/133437  
PRIORITY FILING DATE: 1999-05-11  
PRIORITY APPLICATION NUMBER: 60/133428  
PRIORITY FILING DATE: 1999-05-11  
PRIORITY APPLICATION NUMBER: 60/133438  
PRIORITY FILING DATE: 1999-05-11  
PRIORITY APPLICATION NUMBER: 60/133436  
PRIORITY FILING DATE: 1999-05-11  
PRIORITY APPLICATION NUMBER: 60/137667  
PRIORITY FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 115  
LENGTH: 1861  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-11-031-206-115

Alignment Scores:  
Pred. No.: 4,566-45 Length: 1861  
Score: 541.50 Matches: 171  
Percent Similarity: 46.2% Conservative: 107  
Best Local Similarity: 28.4% Indels: 233  
Query Match: 10.3% Gaps: 91  
DB: 19

US-10-656-394A-8 (1-1032) x US-11-031-206-115 (1-1861)

QY 346 ArgLysThrAsnLysHisGluAspMetGluSerAsnMetGlnLysMetVal 365  
DB 17 AGAAGGGCAATTTTAAATCAATTAAGGACCATGAGTGTCCCGAATCTGTAAGTGGC 76  
QY 366 GluArgLysValAsnLysCysGlyArgLeuProLeuAlaLeuThrLeuGlyAlaVal 385  
DB 77 AAATCTATAGTTGAGGGGTGTGAGGGCTTCCACTAGCAATTTGTCAATAGGCTGCTC 136  
QY 386 LeuAlaThrLysGlnValSerGlu-----TrpGluLysPheTyrGluHisLeuProSer 403  
DB 137 CTGCTTCAAGATCAGGTGCATATATGTTGGATCAATCAATCAATCAATCAATCAAT 196  
QY 404 GluLeuGluAlaAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsn 423  
DB 197 GAGTTGTCAAGAAC-----AATCATGTCCGAGCAATTTTAAATATGAGTACCAT 247  
QY 424 HisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerLeuPheProGluAspPhe 443  
DB 248 GACCTGTAGGAGACCTAAGAACTGCTTTTGTACTGAGGCTTATTCGGAAGACTAC 307  
QY 444 GluLeuLysArgAsnArgLeuValGlyArgTrpLeuAlaGluGlyPheValArgProLys 463  
DB 308 CCCTCTCCGCTGAGAGCCCTTGTGCTGTGGATTGCAAGGCTTTGTCTGAGGAAA 367  
QY 464 ValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuAsnArgSer 483  
DB 368 GAGAACACACACACAGGAGCAGTACGTAGGGAATCTCATGGAATTTGATATACAGGAAT 427  
QY 484 MetIleGlnSerArgValGlyLysAlaGlyLysLysThrCysArgLysHisAsp 503  
DB 428 ATGCTTCAAGTTACAGAGTATGATGATCTCGGAGGGTGAATCTTGTGGAATGATGAC 487  
QY 504 IleLeuArgAspIleThrValSerLysSerArgGlnGluAsnPheValLeuLeuProMet 523

DB 488 ATTATGCGAGACCTGGCCCTTTCTGCTGCTAAAGAGGAGAAGTTT----- 532  
QY 524 GlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMet 543  
DB 533 GGCCTCGCAATGATTTT-----GGCACAATG 559  
QY 544 SerCysLysThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePheGlyAspArg 563  
DB 560 -----GTAGAGATTGAT---AAGGATGTTTCGTCGTCTCAACTACCGATGGAAA 607  
QY 564 ProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAsp 583  
DB 608 GACAGTACT-----GCACCAATCTCAAACTTCTACGCTTCGACCACTAGTATCA 658  
QY 584 LeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCys 603  
DB 659 CTTGAAGCATTTTTCATCTTCATTTGATATGTTGCTCC-----TCAGTTTGTCT 706  
QY 604 HisLeuLysTyrLeuSerIle-----GlyTyrSerSerIleTyrSerLeuProArg 621  
DB 707 CACTCAAGTACCTTACTTGTCTCGAGCTCAAGATTCAGAAATCACTCAAGTCCACCA 766  
QY 622 SerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 641  
DB 767 TCTATAGGGAATTTGTTTAACTTACGTTACATTTGCTTACGGAGGACCAAGGTTAAGTCA 826  
QY 642 LeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPhe 661  
DB 827 CTCCGAGACTCCATTGAAAGTTGCTGAACCTCCACTCTG----- 868  
QY 662 HisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
DB 869 -----GACATGAAG---CAAACAAGATAGAGAAGTCA 898  
QY 682 ProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGluLeu 701  
DB 899 CCACGAGGAATCACT-----AAATCAAGAGCTAAGA----- 931  
QY 702 HisMetAlaThrLysSerCysTrpSerGluSer-----IleGly 714  
DB 932 CACTTGTGTTGCTGATAGATGTTGACGAGACGAGTCCGAGTTCGGATCTTGTAGGA 991  
QY 715 ValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAsp 734  
DB 992 ATGCGAGCACCTTAAAGATCTATCCAACTGAAAGAACTCAAACTCTGGAGACTGTTGAA 1051  
QY 735 IleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLys 754  
DB 1052 GCCAGCAAGGACTTAGCTGAGCAGTTCGAGAACTCATACAACTAAAA----- 1099  
QY 755 LeuGlyValThrThrAsnGlySerThrLysGluLysCysIleLeuTyrAlaIle 774  
DB 1100 ---AGTGTATGATGATGACCAACATGATCTGCTGATTGTGATATATTTTCTACACG 1156  
QY 775 GluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyLysSerAspGlyGly 794  
DB 1157 TCAATATGCCGCTACTTCCAGTTTCTTCTTCTGCAAGGAATGAGAATGAGCACCT 1216  
QY 795 ThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeu 814  
DB 1217 TCTTTTGGGCTCTCAAGCCCAAGTTCCACAGAA-----CTCACAGGTTAATGTC 1267  
QY 815 AspGly-----IleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHis 830  
DB 1268 AGAGGGCAATGGCCACAGAGTACATTGCACTACCCGATATCCATAGCCACAGTACACAT 1327  
QY 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
DB 1328 CTCAAATATTTATCCCTAAGTTGTGTCTCTCGGGAAGATCATTTGGGGAGCTTGGC 1387  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870

Db 1388 TCGAAGCTTGTGGACCTCTACTTATCTAAACCTG---AACCACTGCAGAGTGCAGCAACA 1444  
 Qy 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyGluLeuAsp 890  
 Db 1445 TTAGTTCTTCGTGCAAGGCAATCCCAAACTAAAGACTCTTGTCTTGAGGACAGTGCCT 1504  
 Qy 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
 Db 1505 GATGTCAAGCAGATAAGATCATGTGATGGCGCCCTTCATCCATGATGAATGTTTGTAC--- 1561  
 Qy 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuGlu 930  
 Db 1562 -----ATTGTTGTCTGCGAAGCTGGACAG 1588

Qy 931 IlePro 932

Db 1589 GTCCCT 1594

# RESULT 3

US-11-031-206-109  
 ; Sequence 109, Application US/11031206  
 ; Publication No. US2006003195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Farnodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; PRIOR FILING DATE: 2005-01-07  
 ; PRIOR APPLICATION NUMBER: US/09/566,394  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 109  
 ; LENGTH: 1944  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; US-11-031-206-109

Alignment Scores:  
 Pred. No.: 3,09e-43 Length: 1944  
 Score: 524.00 Matches: 162  
 Percent Similarity: 46.8% Conservative: 107  
 Best Local Similarity: 28.2% Mismatches: 218  
 Query Match: Indels: 88  
 DB: Gaps: 19

US-10-656-394A-8 (1-1032) x US-11-031-206-109 (1-1944)

Qy 375 LeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrIys---GlnValSerGlu 393  
 Db 14 CTGCCACTAGCAATTTGTACAGTCGGCAGCTTCTGTCTCATCTAGACCACAAATAAACATT 73  
 Qy 394 TrpGluLysPheTyGluHisLeuProSerGluLeuGluIleAsnProSerLeuGluAla 413  
 Db 74 TCGAATCAACATCAACACAGCTTCGGAGTGGAGTGTCAACCAAT-----GATCAT 124  
 Qy 414 LeuArgArgMetValThrLeuGlyTyAsnHisLeuProSerHisLeuLysProCysPhe 433  
 Db 125 GTCCGAGCAATCTTAATCTAAGCTACCATGATCTATCTGGAGATCTCAGAAACTGCTTC 184  
 Qy 434 LeuTyLysLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArg 453  
 Db 185 TTGTATTCAGCTTGTTCCTGAAGACTCCCATCTGCAGCGAAGCCCTTGTGGGCTC 244  
 Qy 454 TrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGlu 473  
 Db 245 TGGGTGCGAAGAGTGTCTGAGTAAAGAAAGAAATACACAGAGGAGGTGGCTGAG 304  
 Qy 474 SerTyPheAsnGluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAla 493  
 Db 305 GGAATCTCATGGAATGATCCCGTATATCTTGAAGTTGTAGACTATATGAGCTT 364  
 Qy 494 GlyLysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSer 513  
 Db 365 GGCAGGGTTAGCACTTGCAGATGATCATGAGGAGCTGTCACCTTTGTGTGCC 424  
 Qy 514 ArgGlnGluAsnPheValLeuProMetGlyAspGlySerAspLeu-----529  
 Db 425 AAAGAAGAGAGAGTGT-----GGTTGCAACAGATATATGGTGAAGTATGATA 469  
 Qy 530 ---ValGlnGluAsnThrArgHisIleAlaPheHisGly---SerMetSerCysLysThr 547  
 Db 470 CAGGTGGACACAGAGTTCGTCTGCTTATGTTGGTGAATTTAAAGCAGCAGCT 529  
 Qy 548 GlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly-----561  
 Db 530 AAGTTTAAATTTCCATGTCTCCGACTCTTGTGGCTCAGGGAATATTTTCATCTCTCT 589  
 Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgVal 581  
 Db 590 GACATGGTATCCTCAATTATG-----TCTCAATCAATATTTTTCAGATT 634  
 Qy 582 LeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 601  
 Db 635 CTTGAGCTGCAAGATTTCTGAG-----ATCAGTGGAGTGCCTCA---GCATTTATAGAAAT 685  
 Qy 602 LeuCysHisLeuLysTyLysLeuSerIleGlyTySerSerSerIleTySerLeuProArg 621  
 Db 686 CTCCTTAACCTACGGTATATTTGGTTA---AGCGCACCAAGTCAAGTCACTCCACAG 742  
 Qy 622 SerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIleAlaAla 641  
 Db 743 TCTATTGAGAAGCTCCTCAACCTCCACACTCTCGATATCAAACTCAAACTAGAGAAA 802  
 Qy 642 LeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPhe 661  
 Db 803 CTACCCAGGAGGATTTAGGTCAAGAGCTTAAGCAGCTTTTACCT-----850  
 Qy 662 HisTyAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
 Db 851 -----GACAGGTTTGTCT-----862  
 Qy 682 ProLysValPheThrProLeuValSerArgAspAlaLysGlnIleAlaGluLeu 701  
 Db 863 -----GATGAGACGACGAGGTTTCAGATATTTTC 892  
 Qy 702 HisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGlyIle 721  
 Db 893 -----ATCGAGTGAAGACCTTAAGGCTG 919  
 Qy 722 GlyLysLeuArgAspLeuGlnValLeuGluTyValAspIleArgArgThrSerSerArg 741

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Db 920 TTGAACCTGGAAGAACTACAGACTCTTGAACAGTGCAGGCAAGAACTTGGCTGAA 979
Qy 742 AlaIleGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrLeuGly 761
Db 980 CAGCTGAAGAACTATGCACTGCAAGCTTA-----TGGATCGACAAT 1024
Qy 762 SerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerLeuGln 781
Db 1025 GTAAGCGGTGCAGATTGTGATAACCTTTTCGCGACTCTTCAACCACTGCACTTCTTCC 1084
Qy 782 SerLeuHisValAspAlaAlaGlyIleSerAspGlyThrLeuGluCysLeuAspSer 801
Db 1085 AGCTCTCTAATCTCCGAGAGATGTGAATGAG-----ACACTT---TGCCTCCAGCC 1135
Qy 802 IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyLysLeuGlu----- 819
Db 1136 CTGTCTCCGGAATTTCCAAAGCTCCACAGGCTAATTGTGAAGGGCGCGCTGGCTGCCGAG 1195
Qy 820 -----GluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeu 837
Db 1196 ACATGGAATATCCCAATATTTTGCACCATCGGAACATCTAAATATTTAGCGCTAGC 1255
Qy 838 ArgSerLysLeuGluGlyLysThrMetLeuIleLeuGlyAlaLeuProLeuMet 857
Db 1256 TGGTGCAGCTGGTGAAGATCCATTGGGGTCTCTGCTCGCAGCTGGCGAACCCTCACC 1315
Qy 858 ValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAla 877
Db 1316 TATTTGAGATGAACAGG---GTCAGTAGTCAGACACTTGTGTCTTCTTCGAGGGTGC 1372
Qy 878 PheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluIleArgPhe 897
Db 1373 TTTCCTCACTGAAACACTCTCTCTGAAGAAATGCTCAACGTCGAGCAGCTGGAGATT 1432
Qy 898 GluAspGlySerSerProLeuLeuGluLysIleGluLeuGlyLys----- 913
Db 1433 GGCATGGTGTCTTCCATGTCATCCAAAGTCTGTATCATCATGTCCTAGCGAGCTGGAT 1492
Qy 914 ArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeu 928
Db 1493 AAGGTCCCTCAGGACATGAATCGCTTCTCTCCCTCAAGAAGCTT 1537

RESULT 4
US-11-031-206-137
; Sequence 137, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafaleki, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/11/031,206
; PRIOR FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
```

```
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 137
; LENGTH: 1902
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-11-031-206-137

Alignment Scores:
Pred. No.: 4.32e-38
Score: 474.00
Percent Similarity: 42.0%
Best Local Similarity: 27.7%
Query Match: 9.0%
DB: 25

US-10-656-394A-8 (1-1032) x US-11-031-206-137 (1-1902)
Qy 366 GluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaVal 385
Db 5 GAGGATATTTAAAAAATGTGAGGGTTTACCAGTGGCGATCAATGCCATATCCAGCTTG 64
Qy 386 LeuAlaThr---LysGlnValSerGluTyrGluLysPheTyrGluHisLeuProSerGlu 404
Db 65 TTGCTACTGGGAAACAAAAGAGGTGTATCAGGTTCGAAGCTCTATTGTGTTATGCG 124
Qy 405 LeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsnHis 424
Db 125 CAAAGGAAATTTCTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 184
Qy 425 LeuProSerHisLeuLysProCysPheLeuSerIlePheProGluAspPheGlu 444
Db 185 CTTCCCATCACCCTAAGATATTGCTTATGATGATGATGATGATGATGATGATGATG 244
Qy 445 IleLysArgAsnArgLeuValGlyArgTyrIleAlaGluGlyPheValArgProLysVal 464
Db 245 GTTGAATGGGGCATTAGTACACAGCTGGATTTCTGAGGGTTTGATTCGTGTGAATAT 304
Qy 465 GlyMetThrThrLysAspValGlySerTyrPheAsnGluLeuLeuAsnArgSerMet 484
Db 305 CAGGAAGATCTTGTGGAAATTAGGATATGATATTTAGTAGAGCTTACAAACAGAGTTA 364
Qy 485 IleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIle 504
Db 365 ATGAATCAGTCGGCATGTCAGTATGATGATGATGATGATGATGATGATGATGATGAT 424
Qy 505 IleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGly 524
Db 425 ATCTTGTATTTCTCGTCTAGGTCCGCGAAGAGAAATTTCTGTACCTTTG-----TCA 478
Qy 525 AspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGly-----Ser 542
Db 479 GATAATCCCTCAAGCCAGATCGAAGAGTTCATCGGCTCTCTCTGTTTGGAAATGAAT 538
Qy 543 MetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe----- 560
Db 539 CCATCATGCTCGCACAAATTATGATTTATCGCATGCTCGATCTCTCTGTGTTTGGGCAT 598
Qy 561 ---GlyAspArgProLysSerLeu---AlaHisAlaValCysProAspGlnLeuArgMet 578
Db 599 TCTGGCAATTCCTTCTCTGTCGATGATGATGATGATGATGATGATGATGATGATGAT 634
Qy 579 LeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGln-----LysAspPhe 596
Db 635 CTGCGTGTGCTCGACCTACAAGATTGCCCGAGTTGGGAAATCATCATCATCATCATCAT 694
```





175	Qy	GluMetIleAspThrAsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMet	194
70	Db	GAACATCATGGAGAGTGAGTCACGT-----CTTAAAGTTGTTTCCCAATAATGGAATG	120
195	Qy	GlyGlyLeuGlyIysThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArg	214
121	Db	GGAGGGTGGGTAAGACCAACCTCTTGCCCGTAAGATCCATAACCAACATCAA---GTGCGAG	177
215	Qy	LysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeu	234
178	Db	CTGTGGTTTCCTTGGCTTGGATGGGTTCTGTGTCCACGATTACAGACCCCAAGGAATTT	237
235	Qy	LeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnIleu	254
238	Db	CTTCTCAGCCTTCTCAAAATGCTCAATGTGTCATCCACATCTGAATTTGAAAAATTAAGTGAG	297
255	Qy	LeuGlnGlyLysValValGlnValHisIleuSerGluTyrIleuIleGluGluLeu	274
298	Db	-----GAAGAACTGAAGAAGAGGTAGCGGNAATCGTTTG	330
275	Qy	LysGluLysArgTyrPheValValLeuAspLeuTrp-IleLeuHisAspTrpAsnTrp	294
331	Db	AAAGAGAAGAGGTATCTGTGTAGTCTTGATGACATCTGGGAAACCCCAAGTATGGGATGA	390
294	Qy	PileAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleValIleThrTh	314
391	Db	GGTTAAAGGA--GCCCTTCCA--GATGGCCACACAGGTAGTAGAATACTCATACAAG	444
314	Qy	rArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPh	334
445	Db	TGCGATCAAGAGAGGTGGCATACTATGCTGGAACTGCG--CTTCCCTTACTACCTCCCAT	501
334	Qy	eLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAs	354
502	Db	CCTCAATGAAAAATGAAGCTGGCACTCTTCACAAAGAAGATTTTCGAGGTGAA-----	556
354	Qy	pMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLysCysGlyAr	374
557	Db	----GAATCCCGCTCGATTATAGACCTCTCGGTAGATCCATGTGTGMAAACTGTGGGGG	612
374	Qy	gLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnValSer-----	392
613	Db	TTTACCACCTGCATTGTGTGGTTAGCAGGACTTGTGTGCCAAGAAGGAGAAGTCACAAAG	672
393	Qy	-GluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsnProSerLeuGlu	412
673	Db	AGAGTGGTCAAGAATCAAGGAA-----GTGAGTTGGCGTCTTACACAGGATNAAGA	723
412	Qy	u-AlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProC	432
724	Db	ATCGAGTATGATATGCTGCAACCTTAGGTATGACAACTGCCCTGAAAGATTAATGCCTT	783
432	Qy	yPheLeuTyrLeuSerIlePhePro	440
784	Db	GCCTTTTGTATTTCGAATCTGTCCA	809

## RESULT 6

```

RESULTS: 6
US-11-096-568A-30746
; Sequence 30746, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30746
; LENGTH: 4671
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:

```

Db 1804 AAATCTTTAGACGAAGAAAGAAAGATATTCCTCGACATTCGATGTCTCTTTCTCAAA 1863  
Qy 443 PheGluIleLysArgAsnArgLeuValGlyArgTrrPileAlaGluGlyPheValArgPro 462  
Db 1864 ATGGATATACAAAGAAAGAGTGTGCGAC-----ATACTGAAGGA----- 1905  
Qy 463 LysValGlyMetThrThrLysAspValGlyGluSerThrPheAsnGluLeuLeuAsnArg 482  
Db 1906 ---TGTTGGGTAAACGCC-----GAGGCTGTCTCCGT 1935  
Qy 483 SerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHis 502  
Db 1936 GTTCTTATACAGAAATCTCTCTTACAACTCTTGACAGAC---GACACTGTGTGGATGCAT 1992  
Qy 503 AspIleLeuArgAspIleThrValSerIleSerArgGlnGluAsn-PheValLeuLeuPr 522  
Db 1993 GATCAGATCAGACACATCGGTAGGAGATGGTTTCATAAAGAAAGCAGCATGATCTCTGAG 2052  
Qy 522 oMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySe 542  
Db 2053 ATGGGAGTAGACTCTGGGATCGTG----- 2077  
Qy 542 rMetSerCysLysThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePheGlyAs 562  
Db 2078 -----GTGAATAATGAACGATATTGGACTATATGAAGGGAACATCATCTTCAGGA 2130  
Qy 562 pArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValle 582  
Db 2131 ATCGTACTAGACTTTA-----ATAGAGTTTGGA----- 2161  
Qy 582 uAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 602  
Db 2162 -----GGGACCATACTCGCATGAAATTTCTCGAGTAATC----- 2197  
Qy 602 uCysHisLeuLysThrLeuSerIleGlyTyrrSerSerIleTyrrSerLeuProArgSe 622  
Db 2198 -----TAGCAACATCCGGGTATCTAC-TCTGTATTCATTTACCTGAGAA 2243  
Qy 622 rIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrrIleAlaAla 642  
Db 2244 T-----AAGTTAGTAAGATTTCCAGCAGAGAAAGCCAAAGGCTCTGAATCACCAT 2297  
Qy 642 uProSerGlu-----IleSerLysLeuGlnCysLeuHisThrLeuArgCys11 658  
Db 2298 TCCGTAGATCTTTTGCCACCAATGAAGAGTTGAGACTTCT----- 2340  
Qy 658 eGlyGlnPheHisTyrrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnTh 678  
Db 2341 -----CAGATTAATACGTGGAACTGGAAGAGAGATCTTAAACTTCTCCCATCTGA 2390  
Qy 678 rIle-----CysLeuProLysValPheThrProLeu-----ValSerArgAspAsp 694  
Db 2391 ACTCAAGTGGATACAGTGAAGGTTTC-----CCATTAGAAATCTCCTCCGATATTTCT 2447  
Qy 694 gAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleG1 714  
Db 2448 TTCTAGCAACTTGGTGTCTTGTGACTT-----TCAGAGAGT---GG 2486  
Qy 714 yValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrrValas 734  
Db 2487 AGTAACAGCAGTCAGACTTTGCCCCCAAGGGGAGGAGAGACTTGAAGTTGTA 2546  
Qy 734 pIleArgArgThrSerSer---ArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuAr 753  
Db 2547 TTTGCGTGTGTGCGAGGCTTAGAAGCCATCTCTGATTTATCAAAACATAATGCATAGA 2606  
Qy 753 gLysLeuGlyValThrThrAsnGlySerThrLysGluLysCys----- 767  
Db 2607 AAAGCTT-----GTTCTTGAGCGATGCAACCTTCTGTGTAGAGT 2645  
Qy 768 -----LysIleLeuTyrrAlaAlaIleGluLysLeuSerSe 779  
Db 2646 TCCTAGATCAGTTGGTAAATCTGGGAAATTCCTTCAGCTGAGCCTTAGAAGGTGCTCAAG 2705

Qy 779 rLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLe 799  
Db 2706 TCTTTCTGAATTTCTGGGATGTTTCTGGA-----CTGAAGTGTCT 2747  
Qy 799 uAsp-----SerIleSerSerProPro----- 806  
Db 2748 TGAATAATTTTCTCTCTCTGCTGCTTCAATCTGAGTGTGTTACAGAAACATTCGTTTC 2807  
Qy 807 ----ProLeuLeuArgThrLeuValLeuAspGlyIle----- 817  
Db 2808 CATGCCATGTTTGAAGAGCTTCTCTTGTGAACCTCGCATAGTAAGTAATTCACCGTACTC 2867  
Qy 818 -----LeuGluG1 820  
Db 2868 TATTTTTCGCTCCAAAGCTTGAAGCTTAGTCTAATGGTTCGAGGTCTATTGAAGA 2927  
Qy 820 uMetProAsnTrpIleGluGlnLeuThrHisLeuLysIleTyrrLeuLeuArgSerLy 840  
Db 2928 GCTACCTTCGTGTGAGGATATTTGACATCGCTCGAAGATTATATCTTGTGATGACTGC 2987  
Qy 840 sLeuLysGluGlyLysThrMetLeuLeuGlyAlaLeuProAsnLeuMetValLeuHi 860  
Db 2988 ATTGCGAAACCTTCCTAGTTCT-----ATTGGAGATCTAAATAATCTCCAGAAGCTGCA 3041  
Qy 860 sLeuTyrrArg-----AsnAlaTyrrLeuGlyG1 869  
Db 3042 TCTGATGCGTCGACGCTCCCTTTCTACGATTCCTGAGACTATAATAAGCTCATGTCT 3101  
Qy 869 uLysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrrGlu 889  
Db 3102 GAAGGAATTTATTCATCAATGGAAGC----- 3126  
Qy 889 uAspGlnLeuArgGluLeuArgPheGluAspGlySerSerProLeuLeuGluLysIleG1 909  
Db 3127 ---GGGTTGGAGGAGTACCTATAGAACCGGCTCCTCTCTGTTGACTGACCTCTC 3182  
Qy 909 uIleGlyLysCysArgLeuGluSerGlyIleThrGlyIleHisLeuProLysLeuLy 929  
Db 3183 TCAGAGGATTCGAAATTT-----CTGAA 3206  
Qy 929 sGluIleProLysArgTyrrGlySerLysValAlaGlyLeuGlyGlnLeu 945  
Db 3207 ACAGGTTCCG-----AGTCAATTTGGTGGATTAAATTCCTCT 3243

## RESULT 7

US-11-031-206-101  
; Sequence 101, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; TITLE OF INVENTION: Stress Response  
; FILE REFERENCE: BB1357 US NA  
; CURRENT APPLICATION NUMBER: US/11/031,206  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437

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, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133428
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133438
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133436
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/137667
, PRIOR FILING DATE: 1999-06-04
, NUMBER OF SEQ ID NOS: 208
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 101
, LENGTH: 2382
, TYPE: DNA
, ORGANISM: Zea mays
US-11-031-206-101

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Alignment Scores:		
Pred. No.:	6.22e-21	2382
Score:	.309.00	185
Percent Similarity:	38.5%	154
Best Local Similarity:	20.8%	311
Query Match:	5.9%	241
DB:	9	38
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-656-394A-8 (1-1032) x US-11-031-206-101 (1-2382)

Qy	218	ProCysAsnAlaTriPileThrValSerGlnSerPheHisArgIleGlnLeuLeuLysAsp	237
Db	2	CCACGCGTCCGGAAGATTCCAAATTCAGAGCCCTGAACACACAGTGAGATGCAGCAGACT	61
Qy	238	MetIleArgGlnLeuGlyProSerSerLeuAspGlnLeuLeuGlnGlnLeuGlnGly	257
Db	62	ATCTCCGATAGCTTAATTTGCCATGGAATGAATCAGATAGTTCAGAAA	112
Qy	258	LysValValValGlnValHisIleuSerGluTyrLeuIleGlnGlnLeuLysGluLys	277
Db	113	-----CGGCCAGATTCCTATTGAAGGCACCTGCCAGAA	148
Qy	278	ArgTyrPheValValLeuAspLeu-----TrrIleLeuHisAspTrpAsnTrp	294
Db	149	AGATTTCTATTGCTACTTGTATGAGTAAGGAAGAGATTCGCAGCTGGAGAT	199
Qy	295	IleAsnGluIleAlaPhePro--LysAsnAsnLysLysGlySerArgIleValIleThr	313
Db	200	-----GTCCGTATCCCACTCCGACACGACCAAGCCAAAGCTGATCCTGCACA	250
Qy	314	ThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAsp	333
Db	251	TCACGTTTCCAAGATGCTTCAGATGGGTGCACAGAGAGCCGCAATTGAAATGAAG	310
Qy	334	PheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLys--ThrAsnLysAsnHis	352
Db	311	GTTTTGGATGATAATGCTCCCTGGAACTGTTCTTGAGCAAGCTGACACAGAGCTTTT	370
Qy	353	GluAspMetGluSer-----AsnLysAsnMetGlnLysMetValGluArgIleVal	369
Db	371	GCAGCAGTTTGAGTCACCGAATTTCAACAAGGTTGTTCCGGACACGAGCAAAATATTC	430
Qy	370	AsnLysCysGlyArgLeuPheLeuAlaIleLeuThrIleGly---AlaValLeuAlaThr	388
Db	431	TCCAGTTGTGGAGGCTACCATCTTCATGTGGATGCTGTGGCAGGGGTG	490
Qy	389	LysGlnValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsn	408
Db	491	GAAGGCCAAGATGGATTTTCAGCTGCTAATGATCATC-----AATATGTTTCAGCAAT	544
Qy	409	ProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHis	428
Db	545	GAAAGATGTGGATGAAATGTTTATCCGCTGGAAATACACCTATGACAGGCTGAATCCACT	604
Qy	429	LeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArgAsn	448

Db	605	CAACAACAGTGCCTTTTGTACTGCACCTCTTTTCCCGAAGATATGATCTATATTAGTAAGAA	664
Qy	449	ArgLeuValGlyArgTrrpIleAlaGluGlyPheValArgProLysValGlyMetThr	468
Db	665	CCATTAGTTGATTTTGGCTGGCTGAAGGTTTGGCTT	709
Qy	469	LysAspValGlyGluSerTyrPheAsnGluLeuLeuAsnArgSerMetIleGlnArgSer	488
Db	710	CGTCAAAAGGTGATCAGATAATTCAGACCTTATTTCAGCATGCTGTGTCGACACCGGT	769
Qy	489	ArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAspIle	508
Db	770	AGC---TCATTGTCATCAAAAGTAA---ATGCACCATGTAAATCAGGCATATG	817
Qy	509	ThrVal---SerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySer	527
Db	818	GGCATTTGGTGGTTACACAGACAGATCAAAAGTTCTCGTTCAAGCAGGGATCGCTTTG	877
Qy	528	AspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThr	547
Db	878	GAT-----AGTGCTCCACCA	892
Qy	548	GlyLeuAspTrrpSerIleIleLeuArgSerLeuAlaIlePheGlyAspArgProLysSerLeu	567
Db	893	CGACAAGAGTGGGAAGGAATCGACAAGGATCTCCATCATGCTCTAATGATATCAAAAGCTT	952
Qy	568	AlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAspLeuGluAspVal	587
Db	953	CTTTCTCTCACCG-----GAATGTGAANAACCTC	979
Qy	588	ThrPheLeuIleThrGlnLys-----AspPheAspArgIleAla-	600
Db	980	ACTACATTGTTGATCCAAAATAACCCAAATTTGAACAGCTGAGTTCAGGCTTTTTC	1039
Qy	601	LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro	620
Db	1040	TTTATGCCCTCCTTGAAGAGTGTGATCTTTCTCAC---ACTGCATTAACAACTCCCA	1096
Qy	621	ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla	640
Db	1097	---GAATGTGAGACATTGGTTGCATTACAGCATCTCAATTTGTCACACACAGTATTAGG	1153
Qy	641	AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln	660
Db	1154	TTATTACCT-----GAGCGCTGTGTTATTGAAGAGTTGAGG-----	1192
Qy	661	PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCys	680
Db	1193	---CATCTGGAT-----	1201
Qy	681	LeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGlu	700
Db	1202	-----CTCAGCGTGACTGCTGAA	1219
Qy	701	LeuHisMetAlaThrLysSerCysTrrpSerGluSerIleGlyValLysValProLys---	719
Db	1220	CTCGAAGATACCTTGAACACTGC---TCAAGGTACTCAATTTTAAGAGTTCTTAATCTC	1276
Qy	720	-----GlyIleGlyLysLeuArgAsp-----LeuGlnVal	729
Db	1277	TTTCGCGATCACTATGTTATTAGTGAGCTCAACGACCTGAACTCGAATCTCGATCCCTGA	1336
Qy	730	LeuGluTyrValAspIleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeu	749
Db	1337	CTGATGTTCTTGGAACTCACTATTATTATACAGAGAAGGTGTTAAAGAAACTGAACAGACT	1396
Qy	750	SerLysLeuArgLysLeuGlyValThrThrAsnGlySerThr-----	763
Db	1397	AGTCTTTGGCAAG-----TCAACATATCGTCTGCATCTTAAG	1435
Qy	764	-----LysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGln	781
Db	1436	TACTGTAGAGAATAACGATCGATCGAATCAAAATCTCGCATCTCGACACTTGTCAACTCG	1495

Qy 782 SerLeuHisValAspAlaAlaGlyIleSerAspGlyThrLeuGluCysLeuAspSer 801  
Db 1496 GAGCTGTATGTCGAATCA-----TGTCTATAAT--- 1522  
Qy 802 IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMet 821  
Db 1523 -----CTAAACACACTCTTGTGCTGATCTAGCTGAGCGGCATCA 1561  
Qy 822 ProAsnTrpIleGluGlnLeuThr----- 829  
Db 1562 GATTGAGCGCTGAGCTCTCAGCTTCTCAGTTCTGCTGCGAGAACGTCATTGTT 1621  
Qy 830 -----HisLeuIleYsIleYsIleYsLeuLeuArg-----SerIys 840  
Db 1622 GCACCAAGCGCCCAACATTTTCAGCACATCCGCAAAATGACATTCGATTCGCCCAAG 1681  
Qy 841 LeuIleGluGlyIleYsThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHis 860  
Db 1682 TTGAAGAACATCATCATGGTCTCTAAACTTGAATGCTCGAGAGGCTCGTGGATCCAT 1741  
Qy 861 Leu-----TyrArgAsnAlaIleYr 866  
Db 1742 TGTGATGGTGTGCTGAAGATTCTGAAGACAGACCGGTGATGAGGCGAGAAACAACAAATG 1801  
Qy 867 LeuGlyGlu-----LysLeu 871  
Db 1802 TTGGTTCAGGCTCATCTCTTGAAGACAGGAGATAAAGCGATTGATGTCGTCAAAGT 1861  
Qy 872 ValPheIleYsThr-----GlyAlaPheProAsnLeuArgThrLeuTrpIle 886  
Db 1862 GTGTGAAGAGCGATGACAAATGTCATGCTGAGCTCTCGAACCTGAGATCAATCGTGTG 1921  
Qy 887 TyrGluLeuAspGlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGlu 906  
Db 1922 ACTGATGTCAGAGCGCTGAGAGATATC---TGCAAGCCAGAAATTTTCCAGCTCGAG 1978  
Qy 907 LysIleGluIleGlyCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuPro 926  
Db 1979 ACCATCGGGTGGAGGATGTC-----CCG 2002  
Qy 927 LysLeuIleGluIleProIleArgTyrGlySerIysValAlaGlyLeuGlyGlnLeuGlu 946  
Db 2003 AATCTGAGAGATCCCATCTGAGCAGCAGTACACTGTGGAACTGAGCAGGTCGTC 2062  
Qy 947 GlyGluVal-AsnAlaHisProAsnArgProValLeuLeuMetTyrSerAspArgTyr 966  
Db 2063 GGTTCAGTTGAATGTTGGGAGAAC-----TGGAGTGGGAGGACA-- 2102  
Qy 966 rHisAspLeuGlyAlaGluAlaGluGlySerIleGluValGlnThrAlaAspProVa 986  
Db 2103 -----AGGAGGCGAAGGAGAGAGAGTCTTCATTCATCTGACAGGCCCT 2149  
Qy 986 lProAsp-----AlaGluGlySerValThrValAlaValGluAlaThrAs 1001  
Db 2150 CCGCCCTCCGTTGAGCTGTCTCGCGGTTGCTTGTCTGATTTGGCAGGAGGCTCGTTC 2209  
Qy 1001 pProLeuProGluGlnGluGlyGluSerSer 1011  
Db 2210 AATGCTGCCACGNAATAGCGGTTCCGAACTCT 2240

RESULT 8

US-11-031-206-107  
; Sequence 107, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
FILE REFERENCE: BBI357 US NA  
CURRENT APPLICATION NUMBER: US/11/031.206  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: US/09/566,394  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133427  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 107  
LENGTH: 644  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (277)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (415)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (471)  
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NAME/KEY: unsure  
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LOCATION: (585)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (599)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (605)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (610)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (639)  
US-11-031-206-107  
Alignment Scores:  
Pred. No.: 1.37e-20  
Score: 298.00  
Percent Similarity: 59.0%

Length: 644  
Matches: 63  
Conservative: 39

Best Local Similarity:	36.4%	Mismatches:	57
Query Match:	5.7%	Indels:	14
DB:	9	Gaps:	4

US-10-656-394A-8 (1-1032) x US-11-031-206-107 (1-644)

375 LeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrIys---GlnValSerGlu 393  
Db 1 CTGCCACTAGCAATGTTTACAGCTGGCAGCTTGCTGCATCTAGACCAAAATAAACATT 60  
Qy 394 TrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsnProSerLeuGluAla 413  
Db 61 TGGAAATCAAACATACAACAGCTTCGGAGTGAGTTGTCAACCAAT-----GATCAT 111  
Qy 414 LeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPhe 433  
Db 112 GTCCGAGCAATCTTAAATCTAAGCTTACCATGATCTATCTGGAGATCTTCAGAAACTGCTTTC 171  
Qy 434 LeuTyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArg 453  
Db 172 TTGTATGTGAGCTTGTTTCTCGAGACTTACCCCATGTCAACCGNAGCCCTTGTGCGGCTC 231  
Qy 454 TrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGlu 473  
Db 232 TGGGTGCGAGAGGTTTTGTTCTGAGTAAAGAAAGAATAACACCANAGGAGGTGGCTGAG 291  
Qy 474 SerTyrPheAsnGluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAla 493  
Db 292 GGAATAATCTCATGGAATGTATCACCAGTAATATGCTTGAAGTTGTAGACTATGATGAGCTT 351  
Qy 494 GlyLysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSer 513  
Db 352 GGCAGGTTAGCACITTCGAAGATGCATGATATCATAGGAGCCTTGGCACTTGTGTGTGCC 411  
Qy 514 ArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeu----- 529  
Db 412 AAAAAGAGAGAGTTT-----GGTTCTCGAAACGAATTATGTGTGAACTGATA 456  
Qy 530 ---ValGlnGluAsnThrArgHisIleAlaPheHisGly 541  
Db 457 CAGTGGCAGCAAGAGTTCGTGCTGTGTCGATATGTCGN 495

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RESULT 9
US-11-096-568A-34295
; Sequence 34295, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34295
; LENGTH: 4585
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4585)
; OTHER INFORMATION: Ceres Seq. ID no. 13605763
US-11-096-568A-34295

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Alignment Scores:	1.89e-14	Length:	4585
Pred. No.:	250.00	Matches:	204
Score:	36.8%	Conservative:	196
Percent Similarity:	21.4%	Mismatches:	298
Best Local Similarity:	4.7%	Indels:	304
Query Match:	9	Gaps:	56
na:	na		

115-10-555-394A-8. (1-1032) x 115-11-096-568A-34295 (1-4585)

Qy	72	ileArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPheLysValHisIleGlu	91
Db	61	GTAAACGATGTCATTCAGCAACGATGATCGCTTCCAAAC-----GAG	105
Qy	92	SerGlnThrLeuPheArgGlnLeuValLysLeuA:GluArgHisArgIleAlaIle---	110
Db	106	TCTCAATCAATGGTC-----GAGAGAGCTAGGGTTTCTTGTTATG	144
Qy	111	-----ArgIleHisAsnLeuLysSerArgValGluGluValSerSerArg	125
Db	145	ATTTTACCAGGAACCGTACGGTATCTCTTGACAAGCTCGTAGAGTTCTCGATGCCAG	204
Qy	126	AsnThrArgTyrSerLeuValLysProIle-----SerSerGlyThrGlu	140
Db	205	AAGAACAAAGATCAAGTGGTGGTTCGGGTGTTACGGTGTCAGATCATCAGAGACCGAA	264
Qy	141	-----IleAspMetAspSerTyrAla-----	147
Db	265	TGGCTTAGCGCGCTGGATTCGAAGAGATCTTCATCAGTACACCATTCCAGGAAGAATGT	324
Qy	148	-----GluAspIleArgAsnGlnSerAlaArgAsnValAspGlu-----Ala	161
Db	325	AGTGACTCCAGCTGTGAAGAAGACTGTTAGAGATGTGTATGAGAAGCTCTTTTATATG	384
Qy	162	GluLeuValGlyPheSerAspSerLysLeuArgLeuGluMetIleAspThrAsnAla	181
Db	385	GAACGAATGGGAATA-----TATTCGAGCTCTGGAG---ATTGAGAAATGATT	432
Qy	182	AsnAspGlyProAlaLysValIleCysVal-----ValGlyMetGlyGlyLeuGlyLys	199
Db	433	AACAGCAACCGTTGGACATCCGTTGTGTGGAAATTTGGGGTATGCTCGCATAGGCAAG	492
Qy	200	ThrAlaLeuSerArgLysIlePheCluSerGluGluAspIleArgLysAsnPheProCys	219
Db	493	ACTACACTGTCTAAAGCAGCTCTTTGACCAA-----	522
Qy	220	AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIle	239
Db	523	-----ATGCTGGTGAGTTTGTAGTCTCATTTGCTTTTATGAAGACTACACACC	567
Qy	240	Arg-----GlnLeuLeuGlyProSerSerLeu-----AspGlnLeuLeuGlnGluLeu	255
Db	568	AAAGCTATTCAAGAGAGGGTGTATTGTTTGTCTGGAGGAACAGTTTTTGAAGAAAAAT	627
Qy	256	GlnGlyLys-----ValValValGlnValHisIleLeuSerGluTyrIleLeuIleGlu	273
Db	628	GCTGGTGCTAGTGTACCGTTACGAAATGT-----AGCTTGCTTAGGATAGA	675
Qy	274	LeuLysGluLysArgTyrPheValValLeuAspAspLeu-----	286
Db	676	TTAAACAATAAGAGGGTCTCTGTGTTCTTGATGATGTCGCGAGTCTCTGTTGTGGAG	735
Qy	287	TrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLys	306
Db	736	TCCTTTCTTGGAGGGTTTGACTGGTGTGGT-----CCCAA-----	771
Qy	307	GlySerArgIleValIleThrArgAsnValAspLeuAlaGluLysCysAlaThrAla	326
Db	772	---AGTCTAATCATCATACCTCCAAAGATAAATCGGTGTTTCGCCTTGT---CGAGTC	825
Qy	327	SerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArg	346
Db	826	AATCAAATATACAGGTTCCAGGGTTTAAATGAGAAAGAGCGCTCTTCAACTCTTTC	879
Qy	347	LysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGlu	366
Db	880	TCTTTGTGCGCTATAGACGATATG---GCAGAGCAGAAATCTCCACGAGGGTGCMAATG	936
Qy	367	ArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeu	386
Db	937	AAAGCTTTAAATATGCTAATGGCATCCATTTAGCTCTCAATCTTATGGAGAGACTGT	995



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; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 133
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (511)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (523)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (542)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (547)
; FEATURE:
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; LOCATION: (595)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (602)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (610)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (622)..(623)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (629)
; US-11-031-206-133

Alignment Scores:
Pred. No.:      2,31e-14      Length:      629
Score:          237.50      Matches:      63
Percent Similarity: 55.0%      Conservative: 36
Best Local Similarity: 35.0%      Mismatches:  70
Query Match:     4.5%         Indels:       11
DB:              9           Gaps:         5

US-10-656-394A-8 (1-1032) x US-11-031-206-133 (1-629)

Oy 284 AspAspLeuTrpIleuHisAspTrpAsnTrpIleuValLeuAlaPheProLysAsn 303
Db 2 GATGATGTGGGAATCCAGACATATGCTGATGTCAGT---GCAITTT-----CAG 52
Oy 304 AsnLysGlySerArgIleValIleThrThrArgAsnValLeuAlaGluLysCys 323
Db 53 GGTCTCCAGGAAGCGGTGTATGATCAGACAGCGGAAGATGTGCG---GCTCTT 109
Oy 324 AlaThrAlaSerLeuValTyHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeu 343
Db 110 GCTCTAGTGGCGGTCGCTACAACTCCAGCCATTTGGTGGGACGAGTCATTCAAGCTA 169

344 LeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLys 363
170 TTCTGCTCAAGGGCTTTCCACACACACCTAGACCGCAAGTCCCTCCGAGGCTTGAGAG 229
364 MetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThr-IleG1 383
230 GTGGCTGGTGTAGTTAAGAGGTGTCTATGGCTCCCATTTGACCATTTGATCTTCTGG 289
383 yAlaValLeuAlaThrLysGlnValSerGlu-----TrpGluLysPheTyGluHisLe 401
290 CAGCTATTGTCACGAAGCAGCCGACACAGCAGCTTGGAAATCATGTACATCATCTCT 349
401 u-ProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeuG 421
350 CCGGAGCGCAACTACAGGCAATACCATGTCCAGCTATA-----CTTATCTCTGA 400
421 lyTyAsnHisLeuProSerHisLeuLysProCysPheLeuTyTrpLeuSerIlePheProG 441
401 GCTACCATGACTTGCAGAGGTGATCTCAAGAACTGCTCCTGCTACTGACGCTTGTTCCTG 460
441 luAppPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459
461 AAGACTATGCAATGTCAAGGAGAACTTGTGGGTTGTGGGTTGCTGANGGTTTC 516

RESULT 11
US-11-031-206-139
; Sequence 139, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/11/031,206
; PRIOR FILING DATE: 2005-01-07/566,394
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 139
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (378)
; FEATURE:
; NAME/KEY: unsure
```



LOCATION: (420)  
 NAME/KEY: unsure  
 LOCATION: (456)  
 FEATURE: (456)  
 NAME/KEY: unsure  
 LOCATION: (495)  
 FEATURE: (495)  
 NAME/KEY: unsure  
 LOCATION: (498)  
 FEATURE: (498)  
 NAME/KEY: unsure  
 LOCATION: (506)  
 FEATURE: (506)  
 NAME/KEY: unsure  
 LOCATION: (546)  
 FEATURE: (546)  
 NAME/KEY: unsure  
 LOCATION: (561)  
 FEATURE: (561)  
 NAME/KEY: unsure  
 LOCATION: (567)  
 FEATURE: (567)  
 NAME/KEY: unsure  
 LOCATION: (577)  
 FEATURE: (577)  
 NAME/KEY: unsure  
 LOCATION: (581)  
 FEATURE: (581)  
 NAME/KEY: unsure  
 LOCATION: (583)  
 FEATURE: (583)  
 NAME/KEY: unsure  
 LOCATION: (599)  
 FEATURE: (599)  
 NAME/KEY: unsure  
 LOCATION: (615)  
 FEATURE: (615)  
 NAME/KEY: unsure  
 LOCATION: (621)  
 FEATURE: (621)  
 NAME/KEY: unsure  
 LOCATION: (623)  
 FEATURE: (623)  
 US-11-031-206-139

Alignment Scores:  
 Pred. No.: 4.55e-13  
 Score: 225.00  
 Percent Similarity: 52.4%  
 Best Local Similarity: 35.4%  
 Query Match: 4.3%  
 DB: 9  
 Length: 634  
 Matches: 58  
 Conservative: 28  
 Mismatches: 48  
 Indels: 30  
 Gaps: 6

US-10-656-394A-8 (1-1032) x US-11-031-206-139 (1-634)

Qy 368 IleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAla 387  
 Db 3 ATAGTTGATAGGTGTCATGCTACCTCTAGCAATTGTACCAATTTGGTGCATGTTGCT 62  
 Qy 388 ThrLysGln---ValSerGluTrpGluLysPheTyrgluHisLeuProSerGluLeuGlu 406  
 Db 63 TCAAGACAACGATTAGACATTTGGAAATCAAAATACCAATCAGCTTCGAACGCGAGTTGTCA 122  
 Qy 407 IleAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyraHisLeuPro 426  
 Db 123 AACAAAT-----GATCATGTCGACCAATTTAACTGAGCTACCATGACCTTCCA 173  
 Qy 427 SerHisLeuLysProCysPheLeuTyrgluSerLeuPheProGluAspPheGluLeuLys 446  
 Db 174 GACGACCTCAAAACTGTTTTTATCTGTCAGCTCTATTCCTGAGACTATCACATGTCA 233  
 Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMet 466

Db 234 CCGTGAACCTTGGTGGCTGTGGGTGCGGAGGCTTGGGTAGGTAAGAAAGAAAGAA 293  
 Qy 467 ThrThrLysAsp-----ValGlyGluSerTyrrPheAsnGluLeuIleAsnArgSer 483  
 Db 294 CACACCAGAGATGGTAGCTTGGAGGAACTCC-----ATGGAT 332  
 Qy 484 MetIleGlnArgSerArgValGlyIleAla----- 493  
 Db 333 TTGATCCAAACCGCAATAGCTTTGAAGTTGTTAGAGAATGATGACTTNGTAAGTAACACT 392  
 Qy 494 GlyLysIleLysThrCysArgIleHisAspIleLeuArgAspIleThrValSerIleSer 513  
 Db 393 GGTAAAGTCAATCATATGTCGCGTGAAC-----NACTAGTCCGTTGCT 434  
 Qy 514 ArgGlnGluAsn 517  
 Db 435 AAAGAAGAAAT 446

RESULT 12

US-11-031-206-105  
 ; Sequence 105, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famedu, Omelayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; PRIOR FILING DATE: 2005-01-07  
 ; PRIOR APPLICATION NUMBER: US/09/566,394  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 105  
 ; LENGTH: 1892  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays

US-11-031-206-105

Alignment Scores:  
 Pred. No.: 1.69e-10  
 Score: 206.50  
 Percent Similarity: 34.2%  
 Best Local Similarity: 20.4%  
 Query Match: 3.9%  
 DB: 9  
 Length: 1892  
 Matches: 133  
 Conservative: 90  
 Mismatches: 138  
 Indels: 291  
 Gaps: 33

US-10-656-394A-8 (1-1032) x US-11-031-206-105 (1-1892)

416	QY	ArgMetValThrLeuGlyTyrAsnHisLeuProSer---HisIleuLysProCysPheLeu	434
417	QY		
418	QY		
419	QY		
420	QY		
421	QY		
422	QY		
423	QY		
424	QY		
425	QY		
426	QY		
427	QY		
428	QY		
429	QY		
430	QY		
431	QY		
432	QY		
433	QY		
434	QY		
435	QY	TyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrp	454
436	QY		
437	QY		
438	QY		
439	QY		
440	QY		
441	QY		
442	QY		
443	QY		
444	QY		
445	QY		
446	QY		
447	QY		
448	QY		
449	QY		
450	QY		
451	QY		
452	QY		
453	QY		
454	QY		
455	QY	IleAlaGluGlyPheValArgProLysValGlyMetThrThrIysAspValGlyGluSer	474
456	QY		
457	QY		
458	QY		
459	QY		
460	QY		
461	QY		
462	QY		
463	QY		
464	QY		
465	QY		
466	QY		
467	QY		
468	QY		
469	QY		
470	QY		
471	QY		
472	QY		
473	QY		
474	QY		
475	QY	TyrPheAsnGluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGly	494
476	QY		
477	QY		
478	QY		
479	QY		
480	QY		
481	QY		
482	QY		
483	QY		
484	QY		
485	QY		
486	QY		
487	QY		
488	QY		
489	QY		
490	QY		
491	QY		
492	QY		
493	QY		
494	QY		
495	QY	LysIleLysThrCysArgIleHisAspIleLysArgAspIleThrValSerIleSerArg	514
496	QY		
497	QY		
498	QY		
499	QY		
500	QY		
501	QY		
502	QY		
503	QY		
504	QY		
505	QY		
506	QY		
507	QY		
508	QY		
509	QY		
510	QY		
511	QY		
512	QY		
513	QY		
514	QY		
515	QY	GlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThr	534
516	QY		
517	QY		
518	QY		
519	QY		
520	QY		
521	QY		
522	QY		
523	QY		
524	QY		
525	QY		
526	QY		
527	QY		
528	QY		
529	QY		
530	QY		
531	QY		
532	QY		
533	QY		
534	QY		
535	QY	ArgHisIleAlaPheHis-----ThrGlyLeu-----	540
536	QY		

Db	750	GACCTCAGCATGAGATTGGAAAGTTGGTGCACAAGTGCGGAATGGTGTGATTTTCAGGAG	809
Qy	746	LeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGlu	765
Db	810	CTTAGAGACCCTGGCTAGGCTCAAGGCCCTGGACATCACAAATACATCT-	857
Qy	766	LysCysLysIleLeuTyAlaIalIeGluLysLeuSerSerLeuGlnSerLeuHisVal	785
Db	858	-----GTTGAGGCTCTGGAGCGCTGTCCAGCTCATATCGCCTC-----	896
Qy	786	AspAlaIalGlyIleSerAspGlyThrLeuGluCysLeuAaspSerLieserSerPro	805
Db	897	-----GCTGGTTCACAGAACCCTACTGATAAAGACATGCTCGAGCCTGACAAAG---	947
Qy	806	ProProLeuLeuArgThrLeuValLeuAaspGlyIleLeuGluGluMetPro-----	823
Db	948	-----ATAGAGCTTCTCTCCAGCAAC	968
Qy	824	TripIleGluGlnLeuThrHisLeuLysLysIleTyLeuLeu-----	837
Db	969	CTGTGGAAGAACATGACTTAACCTGMAAGGGTGTGGATTGTTCAGCTGGCGCACTTAGCT	1028
Qy	838	-----GAGGTAATCATCGATAGCAGCAAGAAGCTGTGAATAGCAATGCGCTTCCC	1088
Db	841	LeuLysGluGlyLysThrMetLeu-----IleLeuGlyAlaLeuProAsn	855
Db	1089	TTGCAAGCTCGGGCGGAACCTTGTGCGAGAGAGCAGCCTTACTTCCAACCTCGCAT	1148
Qy	856	LeuMetValLeuHisLeuTyArgAsnaIatyrLeuGlyGluLysLeuValPheLysThr	875
Db	1149	ATCATCTCTCAGGACTGTACAAAG-----GTAAGATCGTCTACAAAGGC	1193
Qy	876	GlyAla-----	877
Db	1194	GGGTGTGTACAGAACTTAGCATCATCTGTTCATCTGTTATGCGCTGGAGAGCTG	1253
Qy	877	-----	877
Db	1254	ATTACTGTTAGTGAAGAACAGACATGGCGGCAAGCGGTGGCGGAGGACAAGTTTCGGCA	1313
Qy	878	-----PheProAsnLeuArgThrLeuTripIleTyxGluLeuAasp	890
Db	1314	GGCTTTAGAGTATCATCACCCCTCCCCCACTCAGGAACCTGTACTCTCATGGTTCGCA	1373
Qy	891	GlnLeuArgGluIleArgPheGluAaspGlySerSer-----ProLeu	904
Db	1374	AGTTCCAGGAGGCTC-----AGCAGCAGCACAATGTACACTGCACCTTCCCCCGCG	1421
Qy	905	LeuGluLysIleGluGlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHis	924
Db	1422	CTGGAGGCTGAAAGTTATCGAGTGC-----	1448
Qy	925	LeuProLysLeuLysGluIleProIleArgTyxGly	936
Db	1449	---CCGAATTTGAGAGAGCTGAAACTCTCAGCTGGG	1481

RESULT 13

US-11-031-206-121

; Sequence 121, Application US/11031206

; Publication No. US20060031959A1

; GENERAL INFORMATION:

; APPLICANT: Rafalski, Antoni

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Sakai, Hajime

; APPLICANT: Fomodu, Omolayo O.

; APPLICANT: Odell, Joan T.

; APPLICANT: Meyers, Blake

; APPLICANT: Thorpe, Catherine

; APPLICANT: Weng, Zude

GENERAL INFORMATION:

APPLICANT: Rafaleski, Antoni  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Falco, Saverio Carl  
 APPLICANT: Sakai, Hajime  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Odell, Joan T.  
 APPLICANT: Meyers, Blake  
 APPLICANT: Thorpe, Catherine  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 FILE REFERENCE: BB1357 US NA  
 CURRENT APPLICATION NUMBER: US/11/031,206  
 CURRENT FILING DATE: 2005-01-07  
 PRIOR APPLICATION NUMBER: US/09/566,394  
 PRIOR FILING DATE: 2000-05-05  
 PRIOR APPLICATION NUMBER: 60/133038  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: 60/133042  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: 60/133427  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133437  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133428  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133438  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133436  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/137667  
 NUMBER OF SEQ ID NOS: 208  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO 121  
 LENGTH: 795  
 TYPE: DNA  
 ORGANISM: Glycine max

Alignment Scores:  
 Pred. No.: 1,03e-10 Length: 795  
 Score: 203.50 Matches: 51  
 Percent Similarity: 57.8% Conservative: 23  
 Best Local Similarity: 39.8% Mismatches: 51  
 Query Match: 3.9% Indels: 3  
 DB: Gaps: 3

US-10-656-394A-8 (1-1032) x US-11-031-206-121 (1-795)

QY 805 ProProLeuLeuArgThrLeuValLeuAspGlyLeuLeuGluGluMetProAsnTrp 824  
 DB 8 CCTCCTCAGTATCTCCAGCAGTATCTTGGTGGGCTAGACAAATTTCCCAATGG 67  
 QY 825 IleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGly 844  
 DB 68 ATAAGTTCTCTCAAGAAATTTGGTCCGAGTGTCTTAAATGAGCGCGGTAGAGAG--- 124  
 QY 845 LysThrMetLeuLeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsn 864  
 DB 125 GATCCTCTGGTACATCTTCAAGATTTGCCAAATCTAGACATCTTGAG---TTTCTTCA 181  
 QY 865 AlaTyrLeuGlyGluLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeu 884  
 DB 182 GTTTATGTTGGTGAGACATCTGCAATTTCAAGCAAAAGGGTTTCTAGTCTGAAGGTGTA 241  
 QY 885 TrpIleTyrGluLeuAspGluLeuArgPheGluAspGlySerSerProLeu 904  
 DB 242 GGCCTGTGATTTAGATGGACTGAATCAATCAATCTGTGGAGGAGGAGCATGCTGGT 301  
 QY 905 LeuGluLysIleGluLeuGlyGluCys---ArgLeuGluSerGlyIleThrGlyIlele 923  
 DB 302 CTTAAAGAGCTCATCATCCAGCGCTGTGATTCATTGAAGCAGGTACCATTAGGCATTGAA 361  
 QY 924 HisLeuProLeuLysGluLeu 931  
 DB 362 CACCTAACAAACTAAATCATATA 385

RESULT 14

US-11-031-206-123/c  
 ; Sequence 123, Application US/11031206  
 ; Publication No. US20060031959A1

GENERAL INFORMATION:

APPLICANT: Rafaleski, Antoni  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Falco, Saverio Carl  
 APPLICANT: Sakai, Hajime  
 APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Odell, Joan T.  
 APPLICANT: Meyers, Blake  
 APPLICANT: Thorpe, Catherine  
 APPLICANT: Weng, Zude  
 TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 FILE REFERENCE: BB1357 US NA  
 CURRENT APPLICATION NUMBER: US/11/031,206  
 CURRENT FILING DATE: 2005-01-07  
 PRIOR APPLICATION NUMBER: US/09/566,394  
 PRIOR FILING DATE: 2000-05-05  
 PRIOR APPLICATION NUMBER: 60/133038  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: 60/133042  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: 60/133427  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133437  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133428  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133438  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/133436  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/137667  
 NUMBER OF SEQ ID NOS: 208  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO 123  
 LENGTH: 306  
 TYPE: DNA  
 ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure  
 LOCATION: (3)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (146)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (156)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (172)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (179)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (219)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (257)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (272)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (290)  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (294)  
 US-11-031-206-123

Alignment Scores:  
 Pred. No.: 1.37e-09 Length: 306

Score:	187.00	Matches:	33
Percent Similarity:	61.5%	Conservative:	15
Best Local Similarity:	42.3%	Mismatches:	30
Query Match:	3.5%	Indels:	0
DB:	9	Gaps:	0

US-10-656-394A-8 (1-1032) x US-11-031-206-123 (1-306)

393	Qy	GluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIleAsnProSerLeuGlu	412
237	Db	GAATGGCAAAAAAATTAGGNGAAGCCTAAAGTTTCAGAGATGAACAAAGATGCCCAATTTAAANT	178
413	Qy	AlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCys	432
177	Db	GGCATWACAAAGATTTTAGGTWTCAGTTATGNTGATTTGCCATATTATCTCGAATCATGC	118
433	Qy	PheLeuTyrLeuSerIleProGluAspPheGluIleLysArgAsnArgLeuValGly	452
117	Db	TTATTGTATTTTGGTGATATCCCGAGACATATGAAGTTAACTCAAAAGATTAAATTTGG	58
453	Qy	ArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrLysAsp	470
57	Db	CAATCGATAGCTGAAGATTTCGTAAAAAGAGGAAGAAGCAAAAACATTATGAGGAC	4

## RESULT 15

```

US-11-031-206-119
; Sequence 119, Application US/11031206
; Publication No. US20060031959A1
;
; GENERAL INFORMATION:
; APPLICANT: Rafaleski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
;
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
;
; FILE REFERENCE: BB1357 US NA
;
; CURRENT APPLICATION NUMBER: US/11/031,206
; CURRENT FILING DATE: 2005-01-07
;
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
;
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
;
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
;
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
;
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
;
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
;
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
;
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
;
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
;
; NUMBER OF SEQ ID NOS: 208
;
; SOFTWARE: Microsoft Office 97
;
; SEQ ID NO 119
; LENGTH: 549

```

```
, , LENGTH: 549  
 , , TYPE: DNA  
 , , ORGANISM: Glycine max  
 , ,  
 , , FEATURE:  
 , , NAME/KEY: unsure  
 , , LOCATION: (402)  
 , ,  
 , , FEATURE:  
 , , NAME/KEY: unsure  
 , , LOCATION: (450)  
 , ,
```

FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(456)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(474)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(492)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(506)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(509)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(518)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(523)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(532)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(541)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(544)
FEATURE:	NAME/KEY:	unsure
NAME/KEY:	LOCATION:	(547)
US-11-031-206-119		

Alignment Scores:			
Pred. No.:	3 498-09	Length:	549
Score:	186.50	Matches:	50
Percent Similarity:	57.5%	Conservative:	23
Best Local Similarity:	39.4%	Mismatches:	50
Query Match:	3.5%	Indels:	4
DR:	9	Gaps:	3

NO 10 555-2048-8 (1-1032) x US-11-031-206-119 (1-549)

Qy	805	ProProLeuLeuArgThrLeuValLeuAspGlyLeuLeuGluMetProAsnThr	824
Db		:            :	
Qy	1	CTCTCTCAGTATCTCCAGCAGTTATACTTGGTGGCGCTCAGACAATTTCCCAATGG	60
Db		:            :	
Qy	825	IleGluGlnLeuThrHisLeuLysGlySyleTyrrLeuLeuArgSerIysLeuLysGluGly	844
Db		:            :	
Qy	61	ATAAGTTCTCTCAAGAATTTGGTCCGAGTGTTCATAAATGGAGCGGTTAGAAAG---	117
Db		:            :	
Qy	845	LysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrrArgAsn	864
Db		:            :	
Qy	118	GATCCTCTCGTATCATCTTCAAGATTTGCCAAATCTAAGACATCTTGAG---	174
Db		:            :	
Qy	865	AlaTyrrLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeu	884
Db		:            :	
Qy	175	GTTTATGTTGGTGAGACATTCGATTTCAAGGCAAAAGGGTTTCTAGTCTGAAGGTGTTA	234
Db		:            :	
Qy	885	TrpIleTyrrGluLeuAspGlnLeu-ArgGluIleArgPheGluAspGlySerSerProLe	904
Db		:::	
Qy	235	GGCCTTGATGATTTAGATGGACTGGAATCATCATCTGTGAGGAGGGAGCATGCTGG	294
Db		:::	
Qy	904	uLeuGluLysIleGluIleGlyGluCys---ArgLeuGlnSerGlyIleThrGlyIleIle	923
Db		:            :	
Qy	295	TCITAAAGACTCATCATCCAGCGCTGTGATTTCATTGAAGCAGGTACCATTTAGGCATTGA	354
Db		:            :	
Qy	923	eHisLeuProLysLeuLys	929
Db		:            :	
Qy	355	ACACCTTAACAAAACATAAA	373
Db		:            :	

Mon Mar 13 10:28:19 2006

us-10-656-394a-8.p2n.rnpbn

Page 18

Search completed: March 9, 2006, 23:56:55  
Job time : 2304 secs